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From: Spector, Lorraine
Sent: Wednesday, September 04, 2002 9:35 AM
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Subject: Serial No. 09/912436

Please search SEQ ID NO:5 and 6

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

-pending
-issued
-commercial

I am interested in hits that are slightly LESS than 100% identical- please print results down to 90% identity, at least.

Also particularly interested in mutations at nucleotides 286-294 of SEQ ID NO:5, if there's any way to search for that specifically.

Thanks.

Lorraine Spector
703-308-1793
U.S. Patent and Trademark Office
Art Unit 1646
lorraine.spector@uspto.gov
CM1-10B11

10D19
~~10B11~~

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Searcher: M. Smith
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Searcher Prep/Review: 10
Clerical: 4
Online time: 10

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 01:51:17 : Search time 24.91 Seconds

(without alignments)
133.355 Million cell updates/sec

Title: US-09-912-436-6

Sequence: 1 MSPLRLRLALALQAPQ.....EEHSCCECRPKKDSAVKPD 136

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

231622

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 99%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	89.6	188	1	US-08-469-427A-5 Sequence 5, Appl1
2	644	89.6	188	2	US-08-609-443B-5 Sequence 5, Appl1
3	644	89.6	188	2	US-08-569-063C-5 Sequence 5, Appl1
4	641	89.2	207	2	US-08-609-443B-13 Sequence 13, Appl1
5	641	89.2	207	2	US-08-569-063C-13 Sequence 13, Appl1
6	630.5	87.7	195	1	US-08-469-427A-7 Sequence 7, Appl1
7	630.5	87.7	195	2	US-08-609-443B-7 Sequence 7, Appl1
8	630.5	87.7	195	2	US-08-569-063C-7 Sequence 7, Appl1
9	612	85.1	133	1	US-08-469-427A-9 Sequence 9, Appl1
10	612	85.1	133	2	US-08-609-443B-9 Sequence 9, Appl1
11	612	85.1	133	2	US-08-569-063C-9 Sequence 9, Appl1
12	489	68.0	102	1	US-08-469-427A-2 Sequence 2, Appl1
13	489	68.0	102	2	US-08-609-443B-2 Sequence 2, Appl1
14	489	68.0	102	2	US-08-569-063C-2 Sequence 2, Appl1
15	269.5	37.5	146	4	US-08-586-039B-33 Sequence 33, Appl1
16	269.5	37.5	146	4	US-08-586-039B-31 Sequence 31, Appl1
17	269.5	37.5	214	4	US-08-586-039B-35 Sequence 35, Appl1
18	266.5	37.1	190	6	5332671-3 Patent No. 5332671
19	264.5	36.8	190	2	US-08-369-063C-20 Sequence 20, Appl1
20	264.5	36.8	231	5	PCT-US96-09001-10 Sequence 10, Appl1
21	264	36.7	147	3	US-08-807-992B-1 Sequence 1, Appl1
22	264	36.7	147	4	US-09-392-932-1 Sequence 1, Appl1
23	264	36.7	191	3	US-08-567-200A-2 Sequence 2, Appl1
24	264	36.7	191	3	US-08-807-992B-2 Sequence 2, Appl1
25	264	36.7	191	3	US-08-691-794-2 Sequence 2, Appl1
26	264	36.7	191	4	US-08-795-430-56 Sequence 56, Appl1
27	264	36.7	191	4	US-09-392-932-3 Sequence 3, Appl1

28	264	36.7	191	6	5332671-4 Patent No. 5332671
29	264	36.7	214	6	5240848-11 Patent No. 5240848
30	264	36.7	215	3	US-08-807-992B-3 Sequence 3, Appl1
31	264	36.7	215	4	US-08-586-039B-49 Sequence 49, Appl1
32	264	36.7	215	6	5240848-7 Patent No. 5240848
33	264	36.7	232	2	US-08-999-811-7 Sequence 7, Appl1
34	264	36.7	232	2	US-08-824-996-9 Sequence 9, Appl1
35	264	36.7	232	2	US-08-807-992B-4 Sequence 4, Appl1
36	264	36.7	232	3	US-09-042-105-7 Sequence 7, Appl1
37	263	36.6	215	6	5219739-22 Patent No. 5219739
38	257	35.7	109	3	US-08-691-794-3 Sequence 3, Appl1
39	257	35.7	110	4	US-09-392-932-11 Sequence 11, Appl1
40	257	35.7	121	6	5194596-19 Patent No. 5194596
41	257	35.7	121	6	5219739-20 Patent No. 5219739
42	257	35.7	145	3	US-08-784-551C-2 Sequence 2, Appl1
43	257	35.7	145	4	US-09-392-932-2 Sequence 2, Appl1
44	257	35.7	165	6	5194596-18 Patent No. 5194596
45	257	35.7	165	6	5219739-19 Patent No. 5219739

ALIGNMENTS

RESULT 1
US-08-469-427A-5
Sequence 5, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alfalo, Kari
APPLICANT: Patiusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
TITLE OF INVENTION: DNA CODING THEREFOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8844
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
SINGLEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-5

Query Match	89.6%	Score 644	DB 1	Length 168	
Best Local Similarity	89.0%	Pred. No. 1.5e-68			
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QY	1 MSPLLRLLALLLQAPAPAVPSQPDAGHGRKVVSWIDVYTRATQCPREVVPPLTVEL	60			
Db	1 MSPLLRLLLVALLQARQAPVSPQDFDSHQKVVPMIDVYARATQCPREVVPPLSMTL	60			
QY	61 MGTAAKQIVPSCVYVQRCGGCCPDGLEGCVPIPGQHOVQRMQIMIRYPSQLGEMSLTEHS	120			
Db	61 MGNVAKQIVPSCVYVQRCGGCCPDGLEGCVPIPGQHOVQRMQIMIRYPSQLGEMSLTEHS	120			
QY	121 QCECRPKKKDSAVKPD	136			
Db	121 QCECRPKKKESAVKPD	136			

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1      RESULT      2
2      US-08-609-443B-5
3      : Sequence 5, Application US/08609443B
4      : Patent No. 5840693
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: ERIKSSON, Ulf
8      : APPLICANT: OLOFSSON, Birgitta
9      : APPLICANT: ALITALO, Kari
10     : APPLICANT: PAUSOLA, Katri
11     :
12     : TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
13     : TITLE OF INVENTION: DNA CODING THEREFOR
14     : NUMBER OF SEQUENCES: 57
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
18     : STREET: 1200 G Street, N.W., Suite 700
19     : CITY: Washington
20     : STATE: DC
21     : COUNTRY: USA
22     : ZIP: 20005
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     : COMPUTER: IBM PC compatible
27     : OPERATING SYSTEM: PC-DOS/MS-DOS
28     : SOFTWARE: Patentin Release #1.0, Version #1.25
29     :
30     : CURRENT APPLICATION DATA:
31     : APPLICATION NUMBER: US/08/609,443B
32     : FILING DATE: 01-MAR-1996
33     : CLASSIFICATION: 435
34     :
35     : PRIOR APPLICATION DATA:
36     : APPLICATION NUMBER: US 08/397,651
37     : FILING DATE: 01-MAR-1995
38     :
39     : PRIOR APPLICATION DATA:
40     : APPLICATION NUMBER: US 08/469,427
41     : FILING DATE: 06-JUN-1995
42     :
43     : PRIOR APPLICATION DATA:
44     : APPLICATION NUMBER: US 08/569,063
45     : FILING DATE: 06-DEC-1995
46     :
47     : ATTORNEY/AGENT INFORMATION:
48     : NAME: EVANS, Joseph D
49     : REGISTRATION NUMBER: 26,269
50     : REFERENCE/DOCKET NUMBER: 1064/41979CP4
51     : TELECOMMUNICATION INFORMATION:
52     : TELEPHONE: (202) 628-8800
53     : TELEFAX: (202) 628-8844
54     :
55     : INFORMATION FOR SEQ ID NO: 5:
56     : SEQUENCE CHARACTERISTICS:
57     : LENGTH: 188 amino acids
58     : TYPE: amino acid
59     : STRANDEDNESS: single
60     : TOPOLOGY: linear
61     : MOLECULE TYPE: protein
62     : HYPOTHETICAL: NO
63     : ORIGINAL SOURCE:
64     : TISSUE TYPE: adult mouse heart
65     :
66     : US-08-609-443B-5

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Query Match	89.6%	Score 644	DB 2	Length 188	
Best Local Similarity	89.0%	Pred. No. 1.5e-68			
Matches 121	Conservative 5	Mismatches 10	Indels 0	Gaps 0	
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Db	1	MSPFLRLRLTLLVALLQARLQAPVSPQDFDSHQKVVPMIDVYARATQCPREVVPLSMEL	60		
QY	61	MGTAAKQLYPSCVYVQRGCGCCPDGGLCEVPLPGHQHVRKQILMIKYPSSQLGEMSLSEHS	120		
Db	61	MGNVVKQOLVPSCVYVQRGCGCCPDGGLCEVPLPGHQHVRKQILMIQYPPSSQLGEMSLSEHS	120		
QY	121	QCECRPKKKDSAVKPD	136		
Db	121	QCECRPKKKESAVKPD	136		

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RESULT      3
US-08-569-063C-5
Sequence 5, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katariina
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-569-063C-5
Query Match      89.6%; Score 644; DB 2; Length 188;
Best Local Similarity 89.0%; Pred. No. 1,5e-68;

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Query Match	89.28;	Score 641;	DB 2;	Length 207;
Best Local Similarity	88.28;	Pred. No. 3.7e-68;		
Matches 120;	Conservative 6;	Mismatches 10;	Indels 0;	Gaps 0

Query Match	89.2%	Score 641	DB 2:	Length 207
Best Local Similarity	88.2%	Pred. No. 3.7e-68		
Matches 120; Conservative	6; Mismatches 10;	Indels 0;	Gaps 0	

Oy 1 MSPLLRRLLAALLQLAPQAQPVSPDPAPGCRKVVSMIDVYTRATCQPREVVPLTVEL 600
||||| ||||| ||||| : | : ||||| ||||| ||||| ||||| : : ||
Db 1 MSPLLRRLLVALLQLARTQAQPAVFDPGSHQKKVPEWIDVYARATCQPREVVVPLSMEL 600

Db 121 MSLEHSCRCRPRKKESAVKPD 143

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RESULT 8
US-08-569-063C-7
; Sequence 7, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-7
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Best Local Similarity 84.6%; Pred. No. 6e-67;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 MSPLRLRLAALLQAPAVSOPDAPGHQKRVSMIDVYTRATCPREVVPVLTVEL 60
Db 1 MSPLRLRLAALLQAPAVSOPDAPGHQKRVSMIDVYTRATCPREVVPVLTVEL 60
QY 61 MGTAKQLVPSCVTVORCGCCPDGDLCEVPTGQHVRM-----QILMIRYPSQGLGE 113
Db 61 MGNVVKQLVPSCVTVORCGCCPDGDLCEVPTGQHVRMVGPRGQILMIRYPSQGLGE 120
QY 114 MSLEHSCRCRPRKKESAVKPD 136
Db 121 MSLEHSCRCRPRKKESAVKPD 143
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RESULT 9
US-08-469-427A-9
; Sequence 9, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-427A-9
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Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPLRLRLAALLQAPAVSOPDAPGHQKRVSMIDVYTRATCPREVVPVLTVEL 60
Db 1 MSPLRLRLAALLQAPAVSOPDAPGHQKRVSMIDVYTRATCPREVVPVLTVEL 60
QY 61 MGTAKQLVPSCVTVORCGCCPDGDLCEVPTGQHVRMQLIMIRYPSQGLGMSLEHSH 120
Db 61 MGNVVKQLVPSCVTVORCGCCPDGDLCEVPTGQHVRMQLIMIRYPSQGLGMSLEHSH 120
QY 121 OCECRPRKK 129
Db 121 OCECRPRKK 129

RESULT 10
US-08-609-443B-9
; Sequence 9, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
```

APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-443B-9

Query Match 85.1%; Score 612; DB 2; Length 133;
Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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DB 1 MSPLRLRLVALLQARQAPYSPDGPSSHQKRVPMIDVYARATCQPREVVPLSMEL 60
QY 61 MGTVAQLVPSCVTYVRCGCGCCPDGDLCEVPTGQHOVHMQLIMIRYPSQLGEMSLSEHS 120
DB 61 MGTVAQLVPSCVTYVRCGCGCCPDGDLCEVPTGQHOVHMQLIMIRYPSQLGEMSLSEHS 120
QY 121 QCECRPKK 129
DB 121 QCECRPKK 129

RESULT 11
US-08-565-063C-9
Sequence 9, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Katri
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-063C-9

Query Match 85.1%; Score 612; DB 2; Length 133;
Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 MSPLRLRLAALLQAPAPYSPDAPGHQKRVSMIDVYTRATCQPREVVPLTVEL 60
DB 1 MSPLRLRLVALLQARQAPYSPDGPSSHQKRVPMIDVYARATCQPREVVPLSMEL 60
QY 61 MGTVAQLVPSCVTYVRCGCGCCPDGDLCEVPTGQHOVHMQLIMIRYPSQLGEMSLSEHS 120
DB 61 MGTVAQLVPSCVTYVRCGCGCCPDGDLCEVPTGQHOVHMQLIMIRYPSQLGEMSLSEHS 120
QY 121 QCECRPKK 129
DB 121 QCECRPKK 129

RESULT 12
US-08-469-427A-2
Sequence 2, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Katri
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington

;; FILING DATE: 06-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 102 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: mouse embryo
US-08-569-063C-2

Query Match 68.0%; Score 489; DB 2; Length 102;
Best Local Similarity 91.8%; Pred. No. 1.4e-50;
Matches 89; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 33 RKVYSWIDYTRATCPREVYVPLTELKGTVAKOLVPSCVTVORCGCCPDGLGCVPT 92
Db 2 RPVPYPIDYARATCPREVYVPLSMLMGNYVKOLVPSCVTVORCGCCPDGLGCVPT 61
Qy 93 GQHVRMQLIMIRYPSQSGEMSLSEHSOCECRPKK 129
Db 62 GQHVRMQLIMIRYPSQSGEMSLSEHSOCECRPKK 98

RESULT 15
US-08-586-039B-33
; Sequence 33, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (908) 594-3905
;; TELEFAX: (908) 594-4720
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 146 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-586-039B-33

Query Match 37.5%; Score 269.5; DB 4; Length 146;
Best Local Similarity 43.8%; Pred. No. 2e-24;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

Qy 10 LALLQLAPAPVPSQPDARQHGR--KYVSWIDYTRATCPREVYVPLTELKGTVAQ 67
Db 12 LALLLYLHAKWSQAPPTGEGOKAHEVVKFMDYVRSYCRPLETVLDFQETPEIEYI 71
Qy 68 LVPSCVTVORCGCCPDGLGCVPTGQHVVRMQLIMIR-YPSQSGEMSLSEHSOCECRP 126
Db 72 FKPSCVPLMRGAGCCNDALGCVPTSESNTVMQIMIRKPHQSHIGMSFLQHSRCECRP 131

Qy 127 KKSDSAVKPD 136
Db 132 KK--DRTKPE 139

RESULT 16
US-08-586-039B-31
; Sequence 31, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,200

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895

RESULT 26
 US-08-795-430-56
 Sequence 56, Application US/08795430
 Patent No. 6130071
 GENERAL INFORMATION:
 APPLICANT: Alltalo, Karl
 APPLICANT: Joukov, Vladimir
 TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
 TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,430
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FI96/00427
 FILING DATE: 01-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/671,573
 FILING DATE: 28-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/601,132
 FILING DATE: 14-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,895
 FILING DATE: 12-JAN-1996

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-430-56

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```

Query Match          36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

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QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELCEVPTGQHVNRQILMIR-YPPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :
DB 72 IFRPSCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEMSLQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

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RESULT 27
US-09-392-932-3
; Sequence 3, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; EARLIER FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 191
; TYPE: PRP
; ORGANISM: Homo Sapiens
; US-09-392-932-3

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Query Match          36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

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QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELCEVPTGQHVNRQILMIR-YPPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :

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DB 72 IFRPSCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEMSLQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

```

```

RESULT 28
5332671-4
; Patent No. 5332671
; APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W.H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,722
; FILING DATE: 04-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 369,424
; FILING DATE: 21-JUN-1989
; APPLICATION NUMBER: 351,117
; FILING DATE: 12-MAY-1989
; SEQ ID NO:4
; LENGTH: 191
; 5332671-4

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Query Match          36.7%; Score 264; DB 6; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

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QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELCEVPTGQHVNRQILMIR-YPPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :
DB 72 IFRPSCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEMSLQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

```

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RESULT 29
5240848-11
; Patent No. 5240848
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; PEDER, JOSEPH
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/337,037
; FILING DATE: 10-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 274,061
; FILING DATE: 21-NOV-1988
; SEQ ID NO:11
; LENGTH: 214
; 5240848-11

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Query Match          36.7%; Score 264; DB 6; Length 214;
Best Local Similarity 43.9%; Pred. No. 1.5e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

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QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELCEVPTGQHVNRQILMIR-YPPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :

```



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1 FILING DATE: 06-JUN-1995
2 CLASSIFICATION:
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: TO BE ASSIGNED
5 FILING DATE: 24-DEC-1997
6 CLASSIFICATION:
7 ATTORNEY/AGENT INFORMATION:
8 NAME: ERIC K. STEFFE
9 REGISTRATION NUMBER: 36,688
10 REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (202)371-2600
13 TELEFAX: (202)371-2540
14 INFORMATION FOR SEQ ID NO: 7:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 232 amino acids
17 TYPE: amino acid
18 STRANDEDNESS: single
19 TOPOLOGY: not relevant
20 MOLECULE TYPE: protein
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Query Match	36.7%;	Score 264;	DB 3;	Length 232;
Best Local Similarity	43.9%;	Pred. No. 1.6e-23;		
Matches 54;	Conservative 21;	Mismatches 44;	Indels 4;	Gaps 2

[illegible]

```

RESULT 37
5219739-22
; Patent No. 5219739
; APPLICANT: FISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDES,
; JOHN C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVESG120 AND
; HVGE1 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
; VASASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVESG120 AND HVGE121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/559,041
; FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 450, 883
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:22:
; LENGTH: 215
5219739-22

Query Match          36.6%; Score 263; DB 6; Length 215;
Best Local Similarity 43.1%; Pred. No. 2e-23;
Matches 53; Conservative 22; Mismatches 44; Indels 4; Gaps 2;

10 LALLQLDAPQAPVPORAPG---NQRKVSMIVTTRATCRPREVVPLVETLMTGTVAK 66
|| || | | : : | | : : || : || | | : | | : | : | :
Db 12 LALLLYLHNAKTSQAAPRAAEAGGQNNHNEVYAFEMDYQRSCHRFETLYLDFGLREIET 71
67 QLVPSCTVYQRCGGCCPRDGLSEVLTGQNOVYMQL-MIRYSSQLGEMSLSEENSOCEER 125
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72 IEPSCVPLRMIRGGCCNBEGLSEVLTESNITMQLALPHQSGNIGEMSLFLOHNKSECR 131

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OY 126 PKK 128
Db 132 PKK 134

RESULT 38

US-08-691-794-3
; Sequence 3, Application US/08691794
; Patent No. 6057428

GENERAL INFORMATION:

APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.

APPLICANT: L. Bing

TITLE OF INVENTION: Variants of Vascular Endothelial Cell

TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their

TITLE OF INVENTION: Production

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/691,794

FILING DATE: 02-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,827

FILING DATE: 25-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/567,200

FILING DATE: 05-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63758/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-691-794-3

Query Match 35.7%; Score 257; DB 3; Length 109;
Best Local Similarity 44.0%; Pred. No. 4.2e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

OY 21 APVSQDPAPGHRKRVSMIDYTRATCPREVVVPLTVELMGTVAKOLVPSCVTVQRGG 80
Db 1 APMAEGGGQNH-HEVVFEMDYQSRYSCHPIETLVDFQEVYDELEYIFKPSCVPLMRGCG 59

OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSQCECRPKK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHQGHIGEMSFLOHNKCECRPKK 108

RESULT 39

US-09-392-932-11
; Sequence 11, Application US/09392932
; Patent No. 6352975

GENERAL INFORMATION:

APPLICANT: Schreiner, George F.

APPLICANT: Johnson, Richard J.

TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND

TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN

FILE REFERENCE: SCIOS.002A

CURRENT APPLICATION NUMBER: US/09/392,932

CURRENT FILING DATE: 1999-09-09

EARLIER APPLICATION NUMBER: 60/099,694

EARLIER FILING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 110

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-392-932-11

Query Match 35.7%; Score 257; DB 4; Length 110;
Best Local Similarity 44.0%; Pred. No. 4.3e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

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OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSQCECRPKK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHQGHIGEMSFLOHNKCECRPKK 108

RESULT 40

5194596-19

Patent No. 5194596

APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN

C.; MITCHELL, RICHARD L.

TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL

GROWTH FACTOR

NUMBER OF SEQUENCES: 32

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/450,883

FILING DATE: 14-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 387,545

FILING DATE: 27-JUL-1989

SEQ ID NO:19

LENGTH: 121

5194596-19

Query Match 35.7%; Score 257; DB 6; Length 121;
Best Local Similarity 44.0%; Pred. No. 4.8e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

OY 21 APVSQDPAPGHRKRVSMIDYTRATCPREVVVPLTVELMGTVAKOLVPSCVTVQRGG 80
Db 1 APMAEGGGQNH-HEVVFEMDYQSRYSCHPIETLVDFQEVYDELEYIFKPSCVPLMRGCG 59

OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSQCECRPKK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHQGHIGEMSFLOHNKCECRPKK 108

RESULT 41
5219739-20
; Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,

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Descriptor

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3	28.4	94.7	1107	4	AB004273 Bos tauru
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5	26.8	89.3	405	6	AR060512 Sequence
6	26.8	89.3	565	6	AR060512 Sequence
7	26.8	89.3	565	6	136626 Sequence 4
8	26.8	89.3	567	10	MM043837 Mus musculu
9	26.8	89.3	624	6	AR060516 Sequence
10	26.8	89.3	795	10	MM048800 Mus musculu
11	26.8	89.3	886	6	AR060511 Sequence
12	26.8	89.3	886	6	136625 Sequence 1
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17	26.8	89.3	174562	2	AC005848 Homo sapi
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19	25.8	86.0	453	10	AF022952 Rattus no
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21	23.6	78.7	591	6	136627 Sequence 6
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28	20.6	68.7	166269	2	AP001187 Homo sapi
29	20.6	68.7	171980	2	AP000928 Homo sapi
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39	20	66.7	275272	2	AC097195 Rattus no
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44	19.6	65.3	136641	9	AC002544 Homo sapi
45	19.6	65.3	166719	9	AC068137 Homo sapi

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REFERENCE      1 (bases 1 to 202)
AUTHORS       Mandriota, S. J. and Pepper, M.S.
TITLE         Direct Submission
JOURNAL       Submitted (16-OCT-1998) Morphology, CMU, 1 rue Michel Servet, 1211
              Geneva 4, Switzerland
FEATURES      location/Qualifiers
              1..202
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              /db_xref="taxon:9913"
              /tissue_type="heart"
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/db_xref="GI:11095134"
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Best Local Similarity 96.7% Pred. No. 0.15;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
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Db 165 CTGGGCACACCAAGTCGAATGCAGATCC 194

RESULT 2
AB004274 1073 bp mRNA linear MAM 12-JAN-2000
LOCUS Bos taurus mRNA for vascular endothelial growth factor B186
DEFINITION precursor, partial cds.
ACCESSION AB004274.1 GI:4850311
VERSION AB004274.1
KEYWORDS vascular endothelial growth factor B186 precursor; vascular endothelial growth factor B186.
SOURCE Bos taurus Heart tissue_l1b:Heart cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yonekura,H., Sakurai,S., Liu,X., Migita,H., Wang,H., Yamagishi,S., Nomura,M., Abedin,M.J., Unoki,H., Yamamoto,Y. and Yamamoto,H.
TITLE Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes.
JOURNAL J. Biol. Chem. 274 (49), 35172-35178 (1999)
MEDLINE 20044783
AUTHORS Liu,X.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1997) Xiaoxu Liu, Kanazawa University School of Medicine, Department of Biochemistry; Takara-machi 13-1, Kanazawa, Ishikawa 920, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:076-265-2181, Fax:076-234-4226)
FEATURES
source Location/Qualifiers
1..1073
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/db_xref="taxon:9913"
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/tissue_l1b="Heart"
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/product="vascular endothelial growth factor B186 precursor"
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/db_xref="GI:4850312"
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/product="vascular endothelial growth factor B186"

ORIGIN

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Best Local Similarity 96.7% Pred. No. 0.14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
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Db 235 CTGGGCACACCAAGTCGAATGCAGATCC 264

RESULT 3
AB004273 1107 bp mRNA linear MAM 12-JAN-2000
LOCUS Bos taurus mRNA for vascular endothelial growth factor B167
DEFINITION precursor, complete cds.
ACCESSION AB004273.1 GI:4850309
VERSION AB004273.1
KEYWORDS vascular endothelial growth factor B167 precursor; vascular endothelial growth factor B167.
SOURCE Bos taurus Heart tissue_l1b:Heart cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yonekura,H., Sakurai,S., Liu,X., Migita,H., Wang,H., Yamagishi,S., Nomura,M., Abedin,M.J., Unoki,H., Yamamoto,Y. and Yamamoto,H.
TITLE Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes.
JOURNAL J. Biol. Chem. 274 (49), 35172-35178 (1999)
MEDLINE 20044783
AUTHORS Liu,X.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1997) Xiaoxu Liu, Kanazawa University School of Medicine, Department of Biochemistry; Takara-machi 13-1, Kanazawa, Ishikawa 920, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:076-265-2181, Fax:076-234-4226)
FEATURES
source Location/Qualifiers
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/protein_id="BAA77685.1"
/db_xref="GI:4850310"
/translation="MSPLLRRLLAVLLQAPQAQVPSQDPAGHGQKKVSMIDYAR ATCQPREVVVPLNMELMGTVAKOLVPSCVTVQRCGGCPDGLCEVPRGQHQVRRQIL MTIYPSQLGEMSL EEHSCRCRPRKRESAVKPDSPRPLCPRCFQRQRDPDPTCHCR CRRSRPLRCGGRGLELNPDRCRCKLAR"
mat_peptide 159..659
BASE COUNT 246 a 368 c 321 g 172 t
ORIGIN

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Best Local Similarity 96.7% Pred. No. 0.14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
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Db 370 CTGGGCACACCAAGTCGAATGCAGATCC 399

RESULT 4
 AR060514 405 bp DNA linear PAT 29-SEP-1999
 LOCUS AR060514 Sequence 8 from patent US 5840693.
 DEFINITION AR060514
 ACCESSION AR060514
 VERSION AR060514.1 GI:5986964
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 405)
 AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
 TITLE Vascular endothelial growth factor-B
 JOURNAL Patent: US 5840693-A 8 24-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..405
 BASE COUNT 93 a 113 c 120 g 79 t
 ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.7;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
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Db 278 CTGGGCAACACCAAGTCGGAATGCAGATCC 307

RESULT 5
 I36628 405 bp DNA linear PAT 13-MAY-1997
 LOCUS I36628 Sequence 8 from patent US 5607918.
 DEFINITION I36628
 ACCESSION I36628
 VERSION I36628.1 GI:2086453
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 405)
 AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
 TITLE Vascular endothelial growth factor-B and DNA coding therefor
 JOURNAL Patent: US 5607918-A 8 04-MAR-1997;
 FEATURES Location/Qualifiers
 source 1..405
 BASE COUNT 93 a 113 c 120 g 79 t
 ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.7;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
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Db 278 CTGGGCAACACCAAGTCGGAATGCAGATCC 307

RESULT 6
 AR060512 565 bp DNA linear PAT 29-SEP-1999
 LOCUS AR060512 Sequence 4 from patent US 5840693.
 DEFINITION AR060512
 ACCESSION AR060512
 VERSION AR060512.1 GI:5986962
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
 TITLE Vascular endothelial growth factor-B

JOURNAL Patent: US 5840693-A 4 24-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..565
 BASE COUNT 120 a 179 c 166 g 100 t
 ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 565;
 Best Local Similarity 93.3%; Pred. No. 0.7;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 273 CTGGGCAACACCAAGTCGGAATGCAGATCC 302

RESULT 7
 I36626 565 bp DNA linear PAT 13-MAY-1997
 LOCUS I36626 Sequence 4 from patent US 5607918.
 DEFINITION I36626
 ACCESSION I36626
 VERSION I36626.1 GI:2086451
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
 TITLE Vascular endothelial growth factor-B and DNA coding therefor
 JOURNAL Patent: US 5607918-A 4 04-MAR-1997;
 FEATURES Location/Qualifiers
 source 1..565
 BASE COUNT 120 a 179 c 166 g 100 t
 ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 565;
 Best Local Similarity 93.3%; Pred. No. 0.7;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 273 CTGGGCAACACCAAGTCGGAATGCAGATCC 302

RESULT 8
 MMU43837 567 bp mRNA linear ROD 16-MAY-1996
 LOCUS MMU43837
 DEFINITION MMU43837
 ACCESSION U43837
 VERSION U43837.1 GI:1314335
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 567)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE Northern blotting of the murine VEGF-related factor gene
 JOURNAL Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
 MEDLINE 96183052
 REFERENCE 2 (bases 1 to 567)
 AUTHORS Hayward,N.K.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
 Oncology Unit, Queensland Institute of Medical Research, Bancroft
 Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,
 Australia
 FEATURES Location/Qualifiers

source

1. .567
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/dev_stage="neonatal"
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61. .564
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/product="mvrf167"

BASE COUNT 121 a 179 c 166 g 101 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 567;
Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 275 CTGGGCAACACCAAGTCGAATGCAGATCC 304

RESULT 3

LOCUS AR060516 624 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 12 from patent US 5840693.

ACCESSION AR060516

VERSION AR060516.1 GI:5986966

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 624)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 12 24-NOV-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 124 a 213 c 173 g 114 t

ORIGIN

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Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccgaagtcggatgcagatcc 30
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Db 275 CTGGGCAACACCAAGTCGAATGCAGATCC 304

RESULT 10

LOCUS MMU48800 795 bp mRNA linear ROD 19-AUG-1996

DEFINITION Mus musculus vascular endothelial growth factor B precursor
(VEGF-B) mRNA, complete cds.

ACCESSION U48800

VERSION U48800.1 GI:1234824

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 795)
AUTHORS Olofsson,B., Pajusola,K., Kaipainen,A., von Euler,G., Jonkv,V.,
Saksela,O., Orpana,A., Pettersson,R.F., Allitalo,K. and Eriksson,U.
TITLE Vascular endothelial growth factor B, a novel growth factor for
endothelial cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
MEDLINE 96197355

REFERENCE 2 (bases 1 to 795)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-1996) Ulf Eriksson, Ludwig Institute for Cancer
Research, Karolinska Institutet, Doktorsringen 12A, Stockholm,
S-171 77, Sweden

FEATURES
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linked heterodimers with VEGF; binds heparin"
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ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 795;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccgaagtcggatgcagatcc 30
||||| ||||||| ||||||| ||||||| |||||||
Db 369 CTGGGCAACACCAAGTCGAATGCAGATCC 398

RESULT 11

LOCUS AR060511 886 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5840693.

ACCESSION AR060511

VERSION AR060511.1 GI:5986961

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 886)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 1 24-NOV-1998;
FEATURES
Location/Qualifiers
1. .886
/organism="unknown"
BASE COUNT 227 a 261 c 226 g 172 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 184 CTGGGCACACACCAAGTCGAGATGCAGATCC 213

RESULT 12
LOCUS 136625 886 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5607918.
ACCESSION 136625
VERSION 136625.1 GI:2086450
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 886)
AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 1 04-MAR-1997;
FEATURES Location/Qualifiers
source 1..886 /organism="unknown"

BASE COUNT 227 a 261 c 226 g 172 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 184 CTGGGCACACACCAAGTCGAGATGCAGATCC 213

RESULT 13
LOCUS MMU52820 896 bp mRNA linear ROD 08-OCT-1996
DEFINITION Mus musculus vascular endothelial growth factor B 186 (VEGF-B)
ACCESSION U52820
VERSION U52820.1 GI:1488260
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 896)
AUTHORS Olofsson,B., Pajusola,K., Kaipainen,A., von Euler,G., Joukov,V.,
Saksela,O., Orpana,A., Petersson,R.F., Alltalo,K. and Eriksson,U.
TITLE Vascular endothelial growth factor B, a novel growth factor for
endothelial cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
MEDLINE 96197355
REFERENCE 2 (bases 1 to 896)
AUTHORS Olofsson,B., Pajusola,K., von Euler,G., Chliov,D., Alltalo,K. and
Eriksson,U.
TITLE Genomic organization of the mouse and human genes for vascular
endothelial growth factor B (VEGF-B) and characterization of a
second splice isoform
J. Biol. Chem. 271 (32), 19310-19317 (1996)
MEDLINE 96325041
REFERENCE 3 (bases 1 to 896)
AUTHORS Eriksson,U., Alltalo,K., Olofsson,B. and Pajusola,K.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-1996) Ulf Eriksson, Ludwig Institute for Cancer
Research, Karolinska Institutet, Doktorsringen 12A, Stockholm S-171

77, Sweden
FEATURES Location/Qualifiers
source 1..896 /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="heart"
/dev_stage="adult"
1..896 /gene="VEGF-B"
95..718 /gene="VEGF-B"
/codon_start=1
/product="vascular endothelial growth factor B 186"
/protein_id="AAC52823.1"
/db_xref="GI:1488261"
/translation="MSPLLRLLVALLQLARQAPYSQFDGSHQKRVVPIWDYAR
ATCPREVVPVPLSMELMGNVKKOLVPCSVVORCGCCPDGLEGVPTGQHOVMQTL
MIOYPSOLDGMSLESHSOCECRPKKESAVKPRVAIPHRPQRPSPGMDSPGAS
SPADIHPTRAPGSSARLAPSAVNALTPGPAADAAASIAKGA"

BASE COUNT 170 a 317 c 254 g 155 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 896;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 369 CTGGGCACACCAAGTCGAGATGCAGATCC 398

RESULT 14
LOCUS MMU43836 1236 bp mRNA linear ROD 04-DEC-1996
DEFINITION Mus musculus VEGF-related factor mvrf186 precursor mRNA, complete
cds.
ACCESSION U43836
VERSION U43836.1 GI:1703480
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1236)
AUTHORS Townsend,S., Lagercrantz,J., Grimmond,S., Sillins,G.,
Nordenskjold,M., Weber,G. and Hayward,N.
TITLE Characterization of the murine VEGF-related factor gene
Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
MEDLINE 96183052
REFERENCE 2 (bases 1 to 1236)
AUTHORS Hayward,N.K.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
Oncology Unit, Queensland Institute of Medical Research, Bancroft
Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,
Australia
COMMENT On Dec 4, 1996 this sequence version replaced gi:1314333.
FEATURES Location/Qualifiers
source 1..1236 /organism="Mus musculus"
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/clone="m175-m1"
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/clone_lib="Stratagene unizap neonatal whole brain cDNA
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/dev_stage="neonatal"
193..816 /note="VEGF-related factor"
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/product="mvrf186 precursor"
/protein_id="AAC52932.1"
/db_xref="GI:1314334"

mat.peptide
256. .813
/translation="MSPLLRLVAILLQLTATAPGSPGEGCHQKVVMDIVAR
ATCGREVVYPLSMELMAGYVLTQVTRGGCCPDGEGCPGQGHVMQILL
MAYQSSDLGEMSEHSCCECPKPKRSVAKPRVVALPHRRPDRSPVPGPGL
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256. .813

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/note="VEGF-related factor"
/product="mvrfl86"

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BASE COUNT	240 a	429 c	340 g	227 t
OBICIN				

ORIG

Query Match	89.38;	Score 26.8;	DB 10;	Length 1236;
Best Local Similarity	93.38;	Pred. No. 0.69;		
Matches 28; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy 1 ctgggcagcaccacgaatccgagatgcagatcc 30
||||| ||||||| |||||||
Db 467 CTGGGCACACCAAGTCCGAGATGCAGATCC 496

RESULT	15			
AC099830				
LOCUS				
DEFINITION	7265 bp	DNA	linear	HTG 22-NOV-2001
	AC099830			
	Homo sapiens chromosome 11 clone RP11-783K16 map 11, LOW-PASS			

ACCESSION	AC099830
VERSION	AC099830.1
KEYWORDS	HTG; HTGS_PHASE0.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Eukaryota: Metazoa: Chordata: Catarrhini: Vertebrata: Euarchosomiformes: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
1 (bases 1 to 77265)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-783K16
Unpublished
2 (bases 1 to 77265)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.

TITLE	Direct Submission
JOURNAL	Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	All repeats were identified using RepeatMasker:

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

 Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIMR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu

 Project Information
 Center project name: I12600
 Center clone name: 783_K_16

NOTE. This record contains 79 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allow overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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*	938	1807:	contig of 870 bp	in length	
*	1908	1907:	gap of 100 bp		
*	2812	2911:	contig of 904 bp	in length	
*	2912	3812:	contig of 901 bp	in length	
*	3813	3912:	gap of 100 bp		
*	3913	4754:	contig of 842 bp	in length	
*	4755	4854:	gap of 100 bp		
*	4855	5710:	contig of 856 bp	in length	
*	5711	5810:	gap of 100 bp		
*	5811	6654:	contig of 884 bp	in length	
*	6695	6794:	gap of 100 bp		
*	6795	7715:	contig of 921 bp	in length	
*	7716	7815:	gap of 100 bp		
*	7816	8681:	contig of 866 bp	in length	
*	8682	8781:	gap of 100 bp		
*	8782	9652:	contig of 871 bp	in length	
*	9653	9752:	gap of 100 bp		
*	9753	10637:	contig of 885 bp	in length	
*	10638	10737:	gap of 100 bp		
*	10738	115956:	contig of 859 bp	in length	
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*	16617	16716:	gap of 100 bp		
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*	17591	17690:	gap of 100 bp		
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*	19607	19706:	gap of 100 bp		
*	19707	205866:	contig of 880 bp	in length	
*	20587	20686:	gap of 100 bp		
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*	21709	22606:	contig of 898 bp	in length	
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*	22707	23613:	contig of 907 bp	in length	
*	23614	23713:	gap of 100 bp		
*	23714	24559:	contig of 846 bp	in length	
*	24560	24659:	gap of 100 bp		
*	24660	25529:	contig of 870 bp	in length	
*	25530	25629:	gap of 100 bp		
*	25630	26489:	contig of 860 bp	in length	
*	26490	26589:	gap of 100 bp		
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*	27586	28437:	contig of 852 bp	in length	
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*	28538	29418:	contig of 881 bp	in length	
*	29419	29518:	gap of 100 bp		
*	29519	30409:	contig of 891 bp	in length	


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* 30510 31404: contig of 895 bp in length
* 31405 31504: gap of 100 bp
* 31505 32396: contig of 892 bp in length
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* 36402 37259: contig of 858 bp in length
* 37260 37359: gap of 100 bp
* 37360 38244: contig of 885 bp in length
* 38245 38344: gap of 100 bp
* 38345 39216: contig of 872 bp in length
* 39217 39316: gap of 100 bp
* 39317 40227: contig of 911 bp in length
* 40228 40327: gap of 100 bp
* 40328 41227: contig of 900 bp in length
* 41228 41327: gap of 100 bp
* 41328 42233: contig of 906 bp in length
* 42234 42333: gap of 100 bp
* 42334 43199: contig of 866 bp in length
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* 43300 44198: contig of 899 bp in length
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* 44299 45157: contig of 859 bp in length
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* 45258 45945: contig of 688 bp in length
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* 47996 48869: contig of 874 bp in length
* 48870 48968: gap of 100 bp
* 48970 49856: contig of 887 bp in length
* 49857 49956: gap of 100 bp
* 49957 50856: contig of 900 bp in length
* 50857 50956: gap of 100 bp
* 50957 51753: contig of 797 bp in length
* 51754 51853: gap of 100 bp
* 51854 52725: contig of 872 bp in length
* 52726 52825: gap of 100 bp
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* 54671 54770: gap of 100 bp
* 54771 55660: contig of 890 bp in length
* 55661 55760: gap of 100 bp
* 55761 56659: contig of 899 bp in length
* 56660 56759: gap of 100 bp
* 56760 57668: contig of 910 bp in length
* 57670 57768: gap of 100 bp
* 57770 58674: contig of 905 bp in length
* 58675 58774: gap of 100 bp
* 58775 59668: contig of 894 bp in length
* 59669 59768: gap of 100 bp
* 59769 60677: contig of 909 bp in length
* 60678 60777: gap of 100 bp
* 60778 61629: contig of 852 bp in length
* 61630 61729: gap of 100 bp
* 61730 62589: contig of 860 bp in length
* 62590 62689: gap of 100 bp
* 62690 63545: contig of 856 bp in length
* 63546 63645: gap of 100 bp
* 63646 64503: contig of 858 bp in length
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* 64604 65475: contig of 872 bp in length
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Query Match
Best Local Similarity 93.3%; Score 26.8; DB 2; Length 77265;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ctggcagcaccagtcgcgatgcagatcc 30
Db 55148 CTGGCAGCACCAAGTCGATCGAGTAC 55177

RESULT 16
AP001453
LOCUS
DEFINITION
Homo sapiens chromosome 11 clone RP11-783K16 map 11q13, WORKING
DRAFT SEQUENCE, 37 unordered pieces.
ACCESSION
AP001453
VERSION
AP001453.3 GI:10130047
KEYWORDS
HTG: HTGS-PARSE1; HTGS-DRAFT.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 151747)
REFERENCE
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 151,747 genomic DNA of 11q13
Published Only in Database (2000) In press
2 (bases 1 to 151747)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Submitted (15-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp URL:http://hnp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Sep 15, 2000 this sequence version replaced gi:8117327.

COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrafl11
Center clone name: RP11-783K16
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136959 bases at least Q40
Consensus quality: 143151 bases at least Q30
Consensus quality: 146210 bases at least Q20
Insert size: 148147, sum-of-contigs
Quality coverage: 8.32x in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently consists of
37 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved.
1 8902 contig of 8902 bp in length
9003 18232 contig of 9230 bp in length
18333 28659 contig of 10337 bp in length
28760 37331 contig of 8572 bp in length
37432 45066 contig of 7635 bp in length
45167 51737 contig of 6571 bp in length
51838 57917 contig of 6080 bp in length
58018 62697 contig of 4680 bp in length

```

62798	66342	contig of	3545	bp	in	length
66443	69246	contig of	2804	bp	in	length
65347	72173	contig of	2827	bp	in	length
72274	76432	contig of	4159	bp	in	length
76533	80848	contig of	4316	bp	in	length
80949	84529	contig of	3581	bp	in	length
84630	88588	contig of	3959	bp	in	length
88689	94224	contig of	5536	bp	in	length
94325	98727	contig of	4403	bp	in	length
98828	102160	contig of	3333	bp	in	length
102261	107715	contig of	5455	bp	in	length
107816	111480	contig of	3665	bp	in	length
111581	114035	contig of	2455	bp	in	length
114136	117720	contig of	3585	bp	in	length
117821	121176	contig of	3356	bp	in	length
121277	123962	contig of	2686	bp	in	length
124063	128424	contig of	4362	bp	in	length
128525	131280	contig of	2756	bp	in	length
131381	133766	contig of	2384	bp	in	length
133865	137166	contig of	3302	bp	in	length
137267	139968	contig of	2702	bp	in	length
140069	141380	contig of	1312	bp	in	length
141481	142715	contig of	1335	bp	in	length
142816	144247	contig of	1432	bp	in	length
144343	146022	contig of	1675	bp	in	length
146123	147416	contig of	1294	bp	in	length
147517	148928	contig of	1410	bp	in	length
149027	150172	contig of	1446	bp	in	length
150273	151747	contig of	1175	bp	in	length.
NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.						
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8903	9002:	gap of	100	bp		
9003	18232:	contig of 9230	bp	in	length	
18233	18332:	gap of	100	bp		
18333	28659:	contig of 10327	bp	in	length	
28660	28759:	gap of	100	bp		
28760	37331:	contig of 8572	bp	in	length	
37332	37431:	gap of	100	bp		
37432	45066:	contig of 7635	bp	in	length	
45067	45166:	gap of	100	bp		
45167	51737:	contig of 6571	bp	in	length	
51738	51837:	gap of	100	bp		
51838	57917:	contig of 6080	bp	in	length	
57918	58011:	gap of	100	bp		
58018	62697:	contig of 4680	bp	in	length	
62698	62797:	gap of	100	bp		
62798	66342:	contig of 3545	bp	in	length	
66343	66442:	gap of	100	bp		
66443	66524:	contig of 2804	bp	in	length	
66524	69346:	gap of	100	bp		
69347	72173:	contig of 2827	bp	in	length	
72174	72273:	gap of	100	bp		
72274	76432:	contig of 4159	bp	in	length	
76433	76532:	gap of	100	bp		
76533	80848:	contig of 4316	bp	in	length	
80849	80948:	gap of	100	bp		
80949	84529:	contig of 3581	bp	in	length	
84530	84629:	gap of	100	bp		
84630	88588:	contig of 3959	bp	in	length	
88589	88688:	gap of	100	bp		
88689	94224:	contig of 5536	bp	in	length	
94225	94324:	gap of	100	bp		
94325	98727:	contig of 4403	bp	in	length	
98728	98828:	gap of	100	bp		
98828	102160:	contig of 3333	bp	in	length	
102161	102260:	gap of	100	bp		

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*	107716	107815:	gap of	100 bp	in	length
*	107816	111460:	contlig of	3665 bp	in	length
*	111481	111580:	gap of	100 bp	in	length
*	111581	114035:	contlig of	2445 bp	in	length
*	114036	114135:	gap of	100 bp	in	length
*	114136	117720:	contlig of	3585 bp	in	length
*	117721	117820:	gap of	100 bp	in	length
*	117821	121176:	contlig of	3356 bp	in	length
*	121177	121276:	gap of	100 bp	in	length
*	121277	121362:	contlig of	2866 bp	in	length
*	123653	124062:	gap of	100 bp	in	length
*	124063	128424:	contlig of	4362 bp	in	length
*	128425	128524:	gap of	100 bp	in	length
*	128525	131280:	contlig of	2756 bp	in	length
*	131281	131380:	gap of	100 bp	in	length
*	131381	133764:	contlig of	2384 bp	in	length
*	133765	133864:	gap of	100 bp	in	length
*	133865	137166:	contlig of	3302 bp	in	length
*	137167	137266:	gap of	100 bp	in	length
*	137267	139668:	contlig of	2702 bp	in	length
*	139669	140068:	gap of	100 bp	in	length
*	140069	141380:	contlig of	1312 bp	in	length
*	141381	141480:	gap of	100 bp	in	length
*	141481	142715:	contlig of	1225 bp	in	length
*	142716	142815:	gap of	100 bp	in	length
*	142816	144247:	contlig of	1432 bp	in	length
*	144248	144347:	gap of	100 bp	in	length
*	144348	146032:	contlig of	1675 bp	in	length
*	146033	146122:	gap of	100 bp	in	length
*	146123	147416:	contlig of	1284 bp	in	length
*	147417	147516:	gap of	100 bp	in	length
*	147517	148926:	contlig of	1410 bp	in	length
*	148927	149026:	gap of	100 bp	in	length
*	149027	150172:	contlig of	1446 bp	in	length
*	150173	150272:	gap of	100 bp	in	length
*	150273	151747:	contlig of	1475 bp	in	length

FEATURES

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58018. .62697
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62798. .66342
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66443. .69246
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72274. .76432
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Best Local Similarity	93.3%;	Pred. No. 0.65;		
Matches 28;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

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Oy      1  ctgggacagaccagtcgagtcgagatcc 30
Db 148127 CTGGGACAGCACCAGATCCGATGCAAGTAC 148156

RESULT 17
AC005848/c
LOCUS
DEFINITION Homo sapiens chromosome 11 clone CIT987SK-1012F4, *** SEQUENCING IN
ACCESSION AC005848
VERSION AC005848.1 GI:3779014
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Smith,D.R.
JOURNAL Sequencing of Human Chromosome 10
REFERENCE
AUTHORS Smith,D.R.
JOURNAL Unpublished
TITLE 2 (bases 1 to 174562)
JOURNAL Direct Submission
COMMENT Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02154, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 4561: contig of 4561 bp in length
* 4562 19077: gap of unknown length
* 19078 30350: contig of 11273 bp in length
* 30351 44866: gap of unknown length
* 44867 58909: contig of 14043 bp in length
* 58910 73424: gap of unknown length
* 73425 90412: contig of 16988 bp in length
* 90413 104927: gap of unknown length
* 104928 130554: contig of 25627 bp in length
* 130555 145069: gap of unknown length
* 145070 174562: contig of 29493 bp in length.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/clone="CIT987SK-1012F4"
BASE COUNT 21150 a 29998 c 29519 g 21315 t 72580 others
ORIGIN

Query Match 89.3%; Score 26.8; DB 2; Length 174562;
Best Local Similarity 93.3%; Pred. No. 0.65;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  ctgggacagaccagtcgagtcgagatcc 30
Db 29612 CTGGGACAGCACCAGATCCGATGCAAGTAC 29583

RESULT 18
AF032925
LOCUS
DEFINITION Rattus norvegicus vascular endothelial growth factor B 186
precursor, mRNA, partial cds.
ACCESSION AF032925
VERSION AF032925.1 GI:2641621
KEYWORDS

SOURCE
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Mandriota,S.J. and Pepper,M.S.
JOURNAL Direct Submission
TITLE Submitted (03-NOV-1997) Morphology, University Medical Center, 1
rie Michel Servet, 1211 Geneva 4, Switzerland
FEATURES
Source
1. 349
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="placenta"
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both strands"
<1..349
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(VRF) 186 precursor; VEGF-B 186 precursor"
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/product="vascular endothelial growth factor B 186
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/db_xref="GI:2641622"
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HOVMQIMIOYPSOIGSEMSLEHSCCECRPKRESAVRPAIVAIPIHHRPQPSVLS
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BASE COUNT 78 a 99 c 104 g 68 t
ORIGIN

Query Match 86.0%; Score 25.8; DB 10; Length 349;
Best Local Similarity 93.1%; Pred. No. 1.9;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2  tgggacagaccagtcgagtcgagatcc 30
Db 127 TGGGACAGCACCAGATCCGATGCAAGTAC 155

RESULT 19
AF022952
LOCUS
DEFINITION Rattus norvegicus vascular endothelial growth factor B mRNA,
partial cds.
ACCESSION AF022952
VERSION AF022952.1 GI:2766601
KEYWORDS
SOURCE Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Well,J., Eschenhagen,T., Mittmann,C. and Scholz,H.
JOURNAL Isolation and characterization of rat vascular endothelial growth
factor B (VEGF-B)
TITLE Unpublished
REFERENCE
AUTHORS Well,J., Eschenhagen,T., Mittmann,C. and Scholz,H.
JOURNAL Submitted (31-AUG-1997) Abteilung Allgemeine Pharmakologie,
Universitaets-Krankenhaus Eppendorf, Martinstr.52, Hamburg 20246,
Germany
FEATURES
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QKGGCCPDGECVPIGQVYRMQIMIQYSSQLGEMSLSEHSQCCEPRKESAV
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BASE COUNT 105 a 126 c 136 g 84 t 2 others

ORIGIN

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Best Local Similarity 93.1%; Pred. No. 1.9;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 20
LOCUS AR060513 591 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5840693.
ACCESSION AR060513
VERSION AR060513.1 GI:5986963
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 591)
AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 6 24-NOV-1998;
FEATURES
source Location/Qualifiers
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BASE COUNT 126 a 186 c 174 g 105 t

ORIGIN

Query Match 78.7%; Score 23.6; DB 6; Length 591;
Best Local Similarity 86.7%; Pred. No. 16;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctgggcagcaccagtcgcggtgcagatcc 30
|||||
Db 278 CTGGGCAACACCAAGTCCGAATCGAGTAC 307

RESULT 21
LOCUS I36627 591 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 6 from patent US 5607918.
ACCESSION I36627
VERSION I36627.1 GI:2086452
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 591)
AUTHORS Eriksson,U., Olofsson,B., Alltalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 6 04-MAR-1997;
FEATURES
source Location/Qualifiers
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BASE COUNT 126 a 186 c 174 g 105 t

ORIGIN

Query Match 78.7%; Score 23.6; DB 6; Length 591;
Best Local Similarity 86.7%; Pred. No. 16;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctgggcagcaccagtcgcggtgcagatcc 30
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Db 278 CTGGGCAACACCAAGTCCGAATCGAGTAC 307

RESULT 22
LOCUS AC098622/c 87421 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus clone CH230-92M16, *** SEQUENCING IN PROGRESS
ACCESSION AC098622
VERSION AC098622.3 GI:17973410
KEYWORDS HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 87421)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,
Alstorks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbarta,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonin,D., Bouck,J.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhaey,C.,
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Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Drepper,H.,
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Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
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Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
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Ogun,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
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Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojupokan,I., Rolfe,M.,
Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
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Thomas,S., Usmani,K., Vasquez,L., Vera-V., Villalob,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,A., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wlecezyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zortilla,S., Nelson,D.,
Weinstock,G. and gldbs.R.

Direct Submission
Unpublished
2 (bases 1 to 87421)
Worley,K.C.
Direct Submission
Submitted (27-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064359.

COMMENT

Center: Baylor College of Medicine

Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc.helpebcm.tmc.edu
----- Project Information
Center project name: GHVU
Center clone name: CH230-92M16
----- Summary Statistics
Assembly program: Phrap; version 0.990329first call to findphraplist
Consensus quality: 65274 bases at least Q40
Consensus quality: 72009 bases at least Q30
Consensus quality: 78781 bases at least Q20
Estimated insert size: 56261; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 0.6x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 52 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 3180: contig of 3180 bp in length
* 3181 3280: gap of unknown length
* 3281 6404: contig of 3124 bp in length
* 6405 6504: gap of unknown length
* 6505 8428: contig of 1924 bp in length
* 8429 8528: gap of unknown length
* 8529 11087: contig of 2559 bp in length
* 11088 11187: gap of unknown length
* 11188 13014: contig of 1827 bp in length
* 13015 13114: gap of unknown length
* 13115 15465: contig of 2351 bp in length
* 15466 17263: gap of unknown length
* 17264 17363: contig of 1698 bp in length
* 17364 20502: contig of 3139 bp in length
* 20503 22851: contig of 2249 bp in length
* 22852 22951: gap of unknown length
* 22952 24526: contig of 1575 bp in length
* 24527 24626: gap of unknown length
* 24627 26619: contig of 1993 bp in length
* 26620 28232: contig of 1513 bp in length
* 28233 28332: gap of unknown length
* 28333 30047: contig of 1715 bp in length
* 30048 30147: gap of unknown length
* 30148 32351: contig of 2204 bp in length
* 32352 32451: gap of unknown length
* 32452 34547: contig of 2096 bp in length
* 34548 34647: gap of unknown length
* 34648 35680: contig of 1033 bp in length
* 35681 35780: gap of unknown length
* 35781 37417: contig of 1637 bp in length
* 37418 37517: gap of unknown length
* 37519 39065: contig of 1548 bp in length
* 39066 39165: gap of unknown length
* 39166 40772: contig of 1607 bp in length
* 40773 40872: gap of unknown length
* 40873 42964: contig of 2092 bp in length
* 42965 43064: gap of unknown length
* 43065 44349: contig of 1285 bp in length
* 44350 44449: gap of unknown length
* 44450 46087: contig of 1638 bp in length
* 46088 46187: gap of unknown length
* 46188 47814: contig of 1627 bp in length
* 47815 47914: gap of unknown length
* 47915 49269: contig of 1355 bp in length

49270 49369: gap of unknown length
49370 50548: contig of 1179 bp in length
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52436 53644: contig of 1209 bp in length
53645 53744: gap of unknown length
53745 54804: contig of 1060 bp in length
54805 54904: gap of unknown length
54905 56452: contig of 1548 bp in length
56453 56552: gap of unknown length
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58030 59058: contig of 1029 bp in length
59059 59158: gap of unknown length
59159 60586: contig of 1428 bp in length
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60687 62056: contig of 1370 bp in length
62057 62156: gap of unknown length
62157 63583: contig of 1427 bp in length
63584 63683: gap of unknown length
63684 65026: contig of 1343 bp in length
65027 65127: gap of unknown length
65128 66522: contig of 1396 bp in length
66523 67819: gap of unknown length
67820 67919: contig of 1197 bp in length
67920 69078: gap of unknown length
69079 69178: contig of 1159 bp in length
69179 70267: gap of unknown length
70268 70367: contig of 1089 bp in length
70368 71457: gap of unknown length
71458 71557: contig of 1090 bp in length
71558 72569: gap of unknown length
72569 72669: contig of 1012 bp in length
72670 74152: gap of unknown length
74153 74252: contig of 1483 bp in length
74253 75490: gap of unknown length
75491 75590: contig of 1238 bp in length
75591 76595: gap of unknown length
76596 76695: contig of 1005 bp in length
76696 78165: gap of unknown length
78166 78265: contig of 1470 bp in length
78266 79481: gap of unknown length
79482 79581: contig of 1216 bp in length
79582 80743: gap of unknown length
80744 80843: contig of 1162 bp in length
80844 81859: gap of unknown length
81860 81959: contig of 1016 bp in length
81960 83220: gap of unknown length
83221 83320: contig of 1261 bp in length
83321 84499: gap of unknown length
84499 84599: contig of 1179 bp in length
84500 86124: gap of unknown length
86124 86224: contig of 1525 bp in length
86225 87421: gap of unknown length
87421 87421: contig of 1197 bp in length.

FEATURES
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/db_xref="taxon:10116"
/clone="CH230-92M16"

BASE COUNT 21196 a 20644 c 20168 g 20216 t 5197 others
ORIGIN

Query Match 75.3%; Score 22.6; DB 2; Length 87421;
Best Local Similarity 86.2%; Pred. No. 40;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 tgggcagcacaagtcgcgagtcagatcc 30
||||| ||||||| ||||||| |||||||
Db 39795 TGGGCACACCAAGTCGGAATGCAGGTAC 39767

RESULT	23																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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[illegible]

LKRLCCRHGLGVKALNEMVLQDIRKNLPGLLGGVGHMSVOLFOGFRDLML
LPIEORYRKDGRLMRLGCGAASFGSSSTAALLET.SNRVLQALQTOATFEVYDITSPAP
VSRSLQDRSRARLRGGOOPADIRGVAKAYDTVREJDTPTOTICDVA5RHRKXGL
TGAVGGVIRQLPPTVYKRLILATEXTSSILGSMRQIYVDAHKDHALMKRSDSAD"

BASE COUNT 1124 a 2128 c 1897 g 1150 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 9; Length 6299;
Best Local Similarity 85.2%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagcactcaagtcgcgcgcgcagatcc 30
|||||
DB 4483 GGCAGACATCATGCTCCGATGAGATCC 4509

RESULT 25
AC084075/c 61633 bp DNA linear HNG 12-OCT-2000
LOCUS Homo sapiens chromosome 11 clone CTD-2380K20 map 11, LOW-PASS
DEFINITION
SEQUENCE SAMPLING.
AC084075
AC084075 GI:10799439
VERSION HTG; HTGS_PHASE0.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 61633)
JOURNAL Birren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE Homo sapiens chromosome 11, clone CTD-2380K20
AUTHORS Unpublished
2 (bases 1 to 61633)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
Bouhagalter,B., Brown,A., Burket,G., Campopiano,A., Castle,A.,
Chapel,Y., Colangelo,M., Collins,A., Cooke,P.,
Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRoque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheters,R., Meldrum,J., Menus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisan,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rodov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Souner,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,U., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.

Direct Submission
Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: I10806
Center clone name: 2380_K_20

NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely

arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be generic and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 663: contig of 663 bp in length
664 763: gap of 100 bp
764 1437: contig of 674 bp in length
1438 1537: gap of 100 bp
1538 2244: contig of 707 bp in length
2245 2344: gap of 100 bp
2345 3028: contig of 684 bp in length
3029 3128: gap of 100 bp
3129 3803: contig of 675 bp in length
3804 3903: gap of 100 bp
3904 4582: contig of 679 bp in length
4583 4682: gap of 100 bp
4683 5371: contig of 689 bp in length
5372 5471: gap of 100 bp
5472 6140: contig of 669 bp in length
6141 6240: gap of 100 bp
6241 6914: contig of 674 bp in length
6915 7014: gap of 100 bp
7015 7686: contig of 672 bp in length
7687 7786: gap of 100 bp
7787 8477: contig of 691 bp in length
8478 8577: gap of 100 bp
8578 9276: contig of 699 bp in length
9277 9376: gap of 100 bp
9377 10046: contig of 670 bp in length
10047 10146: gap of 100 bp
10147 10835: contig of 689 bp in length
10836 10935: gap of 100 bp
10936 11596: contig of 661 bp in length
11597 11696: gap of 100 bp
11697 12380: contig of 684 bp in length
12381 12480: gap of 100 bp
12481 13148: contig of 668 bp in length
13149 13248: gap of 100 bp
13249 13915: contig of 667 bp in length
13916 14015: gap of 100 bp
14016 14693: contig of 678 bp in length
14694 14793: gap of 100 bp
14794 15464: contig of 671 bp in length
15465 15564: gap of 100 bp
15565 16255: contig of 691 bp in length
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17815 17914: gap of 100 bp
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19372 19471: gap of 100 bp
19472 20135: contig of 664 bp in length
20136 20235: gap of 100 bp
20236 20913: contig of 678 bp in length
20914 21013: gap of 100 bp
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21762 22438: contig of 677 bp in length
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23245 23344: gap of 100 bp
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24107 24800: contig of 694 bp in length
24801 24900: gap of 100 bp
24901 25593: contig of 693 bp in length
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25694 26386: contig of 693 bp in length
 * 26387 26486: gap of 100 bp
 * 26487 27136: contig of 650 bp in length
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 * 50567 50666: gap of 100 bp
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 * 51355 51454: gap of 100 bp
 * 51455 52137: contig of 683 bp in length
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 * 52238 52905: contig of 668 bp in length
 * 52906 53006: gap of 100 bp
 * 53006 53685: contig of 680 bp in length
 * 53686 53785: gap of 100 bp
 * 53786 54487: contig of 702 bp in length

Query Match 68.7%: Score 20.6; DB 2: Length 61633;
 Best Local Similarity 85.2%: Pred. No. 2.9e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 ggcagcaccaagtcgagtcgagatcc 30
 Db 12760 GGCAGCACCATGCTCCTCATGAGATCC 12734
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RESULT 26

AC000159 108523 bp DNA linear PRI 04-APR-2001
 LOCUS Homo sapiens Chromosome 11q13 BAC Clone b79g17, complete sequence.
 DEFINITION AC000159
 AC000159
 VERSION AC000159.6 GI:4417315
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Emmert-Buck, M.R., Debelenko, L.V., Zhuang, Z., Lubensky, I.A. and Liotta, L.A.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 108523)
 AUTHORS Weisemann, J. and Boguski, M.S.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936

JOURNAL

AUTHORS Agarwal, S.K., Kester, M., Kim, Y.S., Heppner, C., Dong, Q., Spiegel, A.M., Burns, L.A. and Marx, S.J.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936
 JOURNAL Unpublished
 REFERENCE 4 (bases 1 to 108523)
 AUTHORS Chandrasekharappa, S.C., Guru, S.C., Manickam, P., Olufole, S.-E. and Collins, F.S.

JOURNAL

AUTHORS Wang, Y. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAR-1997) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 REFERENCE 6 (bases 1 to 108523)
 AUTHORS Roe, B.A.

JOURNAL

AUTHORS Direct Submission
 JOURNAL Submitted (09-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 REFERENCE 7 (bases 1 to 108523)
 AUTHORS Roe, B.A.

JOURNAL

AUTHORS Direct Submission
 JOURNAL Submitted (11-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 REFERENCE 8 (bases 1 to 108523)
 AUTHORS Roe, B.A.

JOURNAL

AUTHORS Direct Submission
 JOURNAL Submitted (16-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 REFERENCE 9 (bases 1 to 108523)
 AUTHORS Fu, Y., Pan, H., Wang, Y., Dorman, A.F., Dolance, J.E., Smith, B.T., Meadows, S.M. and Roe, B.A.

JOURNAL

AUTHORS Direct Submission
 JOURNAL Submitted (31-MAR-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA


```

REFERENCE
AUTHORS      10 (bases 1 to 108523)
              Fu, Y., Pan, H., Wang, Y., Dorman, A. F., Dolance, J. E., Smith, B. T.,
              Meadows, S. M., and Roe, B. A.
TITLE        Direct Submission
JOURNAL      Submitted (04-APR-2001) Department of Chemistry And Biochemistry,
              The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
COMMENT      On Mar 16, 1999 this sequence version replaced gi:1388739.
FEATURES
  Source
    1..108523
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="11"
      /map="11q13"
      /clone="b79g17"
BASE COUNT   24680 a 28863 c 28496 g 26484 t
ORIGIN
Query Match 68.7% Score 20.6; DB 9; Length 108523;
Best Local Similarity 85.2%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ggcagcaccagtcgcgatgcagatcc 30
      ||||||| ||| ||| ||| |||
Db 72176 GGCAGCACCAGTCCTCATGGAGATCC 72202

RESULT 27
LOCUS      AP000814 135237 bp DNA linear HTG 31-MAY-2000
DEFINITION Homo sapiens chromosome 11 clone xypac-969D11 map 11q13, WORKING
DRAFT SEQUENCE, 31 unordered pieces.
ACCESSION  AP000814
VERSION     AP000814.2 GI:8131587
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens DNA, clone:xypac-969D11.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 135237)
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Homo sapiens 135,237 genomic DNA of 11q13
            Published Only in Database (1999) In press
            2 (bases 1 to 135237)
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Submitted (30-NOV-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamiharu, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hnp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
            On May 31, 2000 this sequence version replaced gi:16997651.

COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Web Site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humpdraft11
Center clone name: XYPAC-969D11
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 116075 bases at least Q40
Consensus quality: 124675 bases at least Q30
Consensus quality: 129566 bases at least Q20
Insert size: 13237; sum-of-contigs

```

```

NOTE: This is a 'working draft' sequence. It currently consists of
31 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved.

-----
Quality coverage: 4.10x in Q20 bases; sum-of-contigs

1
1463 14762 contig of 14762 bp in length
22848 22747 contig of 7885 bp in length
31978 31877 contig of 9030 bp in length
40889 40788 contig of 8811 bp in length
50363 50262 contig of 9374 bp in length
56411 56310 contig of 5348 bp in length
56411 61057 contig of 4647 bp in length
61158 68219 contig of 7062 bp in length
68320 74590 contig of 6271 bp in length
74691 79328 contig of 4502 bp in length
84031 88711 contig of 4681 bp in length
88812 93006 contig of 4195 bp in length
93107 97278 contig of 4172 bp in length
97379 101644 contig of 4466 bp in length
101745 103787 contig of 2043 bp in length
103888 106271 contig of 2384 bp in length
106372 110210 contig of 3839 bp in length
110311 112278 contig of 368 bp in length
112379 114714 contig of 2336 bp in length
114815 117772 contig of 2258 bp in length
117873 120347 contig of 2475 bp in length
120448 121697 contig of 1250 bp in length
121798 123307 contig of 2110 bp in length
124008 125646 contig of 1639 bp in length
125747 127154 contig of 1408 bp in length
127255 129449 contig of 2195 bp in length
129550 130823 contig of 1274 bp in length
130924 132904 contig of 1274 bp in length
133005 134058 contig of 1054 bp in length
134159 135237 contig of 1079 bp in length

Sequence updated (26-May-2000).
NOTE: This is a 'working draft' sequence. It currently
consists of 31 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of 'N', but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1
14763 14862 contig of 14762 bp in length
14863 22747 contig of 7885 bp in length
22748 22847 contig of 100 bp in length
22848 31877 contig of 9030 bp in length
31878 31977 contig of 100 bp in length
31978 40788 contig of 8811 bp in length
40789 40888 contig of 100 bp in length
40889 50262 contig of 9374 bp in length
50263 50362 contig of 100 bp in length
50363 56310 contig of 5348 bp in length
56311 56410 contig of 100 bp in length
56411 61057 contig of 4647 bp in length
61058 61157 contig of 100 bp in length
61158 68219 contig of 7062 bp in length
68220 68319 contig of 100 bp in length
68320 74590 contig of 6271 bp in length
74591 74690 contig of 100 bp in length
74691 79328 contig of 4638 bp in length
79329 79428 contig of 100 bp in length
79429 83930 contig of 4502 bp in length
83931 84030 contig of 100 bp in length
84031 88711 contig of 4681 bp in length
88712 88811 contig of 100 bp in length

```

```

* 88812 93006: contig of 4195 bp in length
* 93007 93106: gap of 100 bp in length
* 93107 97278: contig of 4172 bp in length
* 97279 97378: gap of 100 bp in length
* 97379 101644: contig of 4266 bp in length
* 101645 101744: gap of 100 bp in length
* 101745 103787: contig of 2043 bp in length
* 103788 103887: gap of 100 bp in length
* 103888 106271: contig of 2384 bp in length
* 106272 106371: gap of 100 bp in length
* 106372 110210: contig of 3839 bp in length
* 110211 110310: gap of 100 bp in length
* 110311 112278: contig of 1968 bp in length
* 112279 112378: gap of 100 bp in length
* 112379 114714: contig of 2336 bp in length
* 114715 114814: gap of 100 bp in length
* 114815 117772: contig of 2958 bp in length
* 117773 117872: gap of 100 bp in length
* 117873 120347: contig of 2475 bp in length
* 120348 120447: gap of 100 bp in length
* 120448 121697: contig of 1250 bp in length
* 121698 121797: gap of 100 bp in length
* 121798 123907: contig of 2110 bp in length
* 123908 124007: gap of 100 bp in length
* 124008 125646: contig of 1639 bp in length
* 125647 125746: gap of 100 bp in length
* 125747 127154: contig of 1408 bp in length
* 127155 127254: gap of 100 bp in length
* 127255 129449: contig of 2195 bp in length
* 129450 129549: gap of 100 bp in length
* 129550 130823: contig of 1274 bp in length
* 130824 130923: gap of 100 bp in length
* 130924 132904: contig of 1981 bp in length
* 132905 133004: gap of 100 bp in length
* 133005 134058: contig of 1054 bp in length
* 134059 134158: gap of 100 bp in length
* 134159 135237: contig of 1079 bp in length.

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FEATURES

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   /clone="XPac-969D11"
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   /note="assembly_fragment"
   22848..31877
misc_feature
   /note="assembly_fragment"
   31978..40788
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Query Match      68.7%  Score 20.6; DB 2; Length 135237;
Best Local Similarity 85.2%  Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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```

Oy 4 ggcagcaccagtcgcgatcgatcc 30
||||| 11111111111111111111
Db 119819 GCGAGCACCATGTCTCATGAGATCC 119845

```

```

RESULT 28
AP001187/c 166269 bp DNA linear HTG 17-JAN-2001
LOCUS Homo sapiens chromosome 11 clone RP11-665N17 map 11q13, WORKING
DEFINITION DRAFT SEQUENCE, 27 unordered pieces.
ACCESSION AP001187.3 GI:12245852
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens DNA, clone:RP11-665N17.
SOURCE Homo sapiens
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 166269)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 166,269 genomic DNA of 11q13
Published Only in Database (2000) In press
2 (bases 1 to 166269)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (18-FEB-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jan 16, 2001 this sequence version replaced gi:8117633.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrafi11
Center clone name: RP11-665N17
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 156782 bases at least Q40
Consensus quality: 160361 bases at least Q30
Consensus quality: 162264 bases at least Q20
Insert size: 163669; sum-of-contigs
Quality coverage: 8.32x in Q20 bases; sum-of-contigs

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
COMMENT

```

NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be

```

preserved
1
28395 contig of 28395 bp in length
28496 43446 contig of 14951 bp in length
43547 58083 contig of 14537 bp in length
58184 66868 contig of 8685 bp in length
66969 76574 contig of 9606 bp in length
76675 86418 contig of 9744 bp in length
86519 94044 contig of 7526 bp in length
94145 100790 contig of 6646 bp in length
100891 108539 contig of 7649 bp in length
108640 115961 contig of 7322 bp in length
116062 120258 contig of 4197 bp in length
120359 125359 contig of 5001 bp in length
125460 130186 contig of 4727 bp in length
130287 134400 contig of 4114 bp in length
134501 139064 contig of 4564 bp in length
139065 143906 contig of 4742 bp in length
143907 144006 contig of 100 bp in length
144007 148280 contig of 4274 bp in length
148281 148380 contig of 100 bp in length
148381 151006 contig of 2626 bp in length
151007 153748 contig of 2642 bp in length

NOTE: This is a 'working draft' sequence. It currently
consists of 27 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
28395: contig of 28395 bp in length
28396 28495: gap of 100 bp
28496 43446: contig of 14951 bp in length
43447 43546: gap of 100 bp
43547 58083: contig of 14537 bp in length
58084 58183: gap of 100 bp
58184 66868: contig of 8685 bp in length
66869 66968: gap of 100 bp
66969 76574: contig of 9606 bp in length
76575 76674: gap of 100 bp
76675 86418: contig of 9744 bp in length
86419 86518: gap of 100 bp
86519 94044: contig of 7526 bp in length
94045 94144: gap of 100 bp
94145 100790: contig of 6646 bp in length
100791 100890: gap of 100 bp
100891 108539: contig of 7649 bp in length
108540 108639: gap of 100 bp
108640 115961: contig of 7322 bp in length
115962 116061: gap of 100 bp
116062 120258: contig of 4197 bp in length
120259 120358: gap of 100 bp
120359 125359: contig of 5001 bp in length
125360 125459: gap of 100 bp
125460 130186: contig of 4727 bp in length
130187 130286: gap of 100 bp
130287 134400: contig of 4114 bp in length
134401 134500: gap of 100 bp
134501 139064: contig of 4564 bp in length
139065 139164: gap of 100 bp
139165 143906: contig of 4742 bp in length
143907 144006: gap of 100 bp
144007 148280: contig of 4274 bp in length
148281 148380: gap of 100 bp
148381 151006: contig of 2626 bp in length
151007 153748: contig of 2642 bp in length
```

```

* 153749 153848: gap of 100 bp
* 153849 155555: contig of 1707 bp in length
* 155556 155655: gap of 100 bp
* 155656 157198: contig of 1543 bp in length
* 157199 157298: gap of 100 bp
* 157299 159872: contig of 2574 bp in length
* 159873 159972: gap of 100 bp
* 159973 161499: contig of 1527 bp in length
* 161500 161599: gap of 100 bp
* 161600 162703: contig of 1104 bp in length
* 162704 162803: gap of 100 bp
* 162804 163847: contig of 1044 bp in length
* 163848 163947: gap of 100 bp
* 163948 165121: contig of 1174 bp in length
* 165122 165221: gap of 100 bp
* 165222 166269: contig of 1048 bp in length.
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/chromosome="11"
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/note="assembly_fragment"
58184.66868
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/note="assembly_fragment"
76675.86418
/note="assembly_fragment"
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134501.139064
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144007.148280
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159973.161499
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/note="assembly_fragment"
162804.163847
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misc-feature 165222. .166269 /note="assembly-fragment"
BASE COUNT 37933 a 44411 c 44369 g 36956 t 2600 others
Query Match 68.7%; Score 20.6; DB 2; Length 166269;
Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 ggcagcaccagtcgcgagcagatcc 30
Db 56114 GGCAGCACCATGTCCTCATGAGATCC 56088
RESULT 29
AP000928/c
LOCUS AP000928 171980 bp DNA linear HMG 30-MAY-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-772K10 map 11q13, WORKING
DRAFT SEQUENCE, 33 unordered pieces.
ACCESSION AP000928
VERSION AP000928.2 GI:8119069
KEYWORDS HTG; HMGs_PHASE1; HMGs_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-772K10.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171980)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
Homo sapiens 171,980 genomic DNA of 11q13
2 (bases 1 to 171980)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
Direct Submission
Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997744.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-772K10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14109 bases at least Q40
Consensus quality: 154862 bases at least Q30
Consensus quality: 163556 bases at least Q20
Insert size: 166780; sum-of-contigs
Quality coverage: 3.98x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
33 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 13598 contig of 13598 bp in length
13699 26815 contig of 13117 bp in length
26916 37862 contig of 10947 bp in length
37963 46388 contig of 8426 bp in length
46489 55060 contig of 8572 bp in length

55161 61498 contig of 6338 bp in length
61599 68961 contig of 7263 bp in length
69062 76353 contig of 7292 bp in length
76454 84390 contig of 7937 bp in length
84491 91104 contig of 6614 bp in length
91205 97347 contig of 6143 bp in length
97448 103810 contig of 6636 bp in length
103911 110422 contig of 6512 bp in length
110523 116801 contig of 6279 bp in length
116902 121989 contig of 5088 bp in length
122090 125946 contig of 3857 bp in length
126047 132109 contig of 6063 bp in length
132210 136422 contig of 4213 bp in length
136423 136522 contig of 100 bp in length
61498 contig of 6338 bp in length
68961 contig of 7263 bp in length
76353 contig of 7292 bp in length
84390 contig of 7937 bp in length
91104 contig of 6614 bp in length
97347 contig of 6143 bp in length
103810 contig of 6636 bp in length
110422 contig of 6512 bp in length
116801 contig of 6279 bp in length
121989 contig of 5088 bp in length
125946 contig of 3857 bp in length
132109 contig of 6063 bp in length
136422 contig of 4213 bp in length
136522 contig of 100 bp in length
13598: contig of 13598 bp in length
13699: gap of 100 bp
26815: contig of 13117 bp in length
26916: gap of 100 bp
37862: contig of 10947 bp in length
37963: gap of 100 bp
46388: contig of 8426 bp in length
46489: gap of 100 bp
55060: contig of 8572 bp in length
55061: gap of 100 bp
55161: gap of 100 bp
61498: contig of 6338 bp in length
61499: gap of 100 bp
61599: gap of 100 bp
68961: contig of 7363 bp in length
68962: gap of 100 bp
69062: gap of 100 bp
76353: contig of 7292 bp in length
76354: gap of 100 bp
76454: gap of 100 bp
84390: contig of 7937 bp in length
84391: gap of 100 bp
91104: contig of 6614 bp in length
91205: gap of 100 bp
97347: contig of 6143 bp in length
97348: gap of 100 bp
103810: contig of 6636 bp in length
103811: gap of 100 bp
110422: contig of 6512 bp in length
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116801: contig of 6279 bp in length
116802: gap of 100 bp
121989: contig of 5088 bp in length
121990: gap of 100 bp
125946: contig of 3857 bp in length
125947: gap of 100 bp
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132110: gap of 100 bp
136422: contig of 4213 bp in length
136423: gap of 100 bp

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* 140567 140566: gap of 100 bp in length
* 140667 144574: contig of 3808 bp in length
* 144575 144674: gap of 100 bp in length
* 144675 148311: contig of 3637 bp in length
* 148312 148311: gap of 100 bp in length
* 148412 150652: contig of 2241 bp in length
* 150653 150755: gap of 100 bp in length
* 150755 153335: contig of 2583 bp in length
* 153336 153435: gap of 100 bp in length
* 153436 155668: contig of 2233 bp in length
* 155669 155768: gap of 100 bp in length
* 155769 158851: contig of 3083 bp in length
* 158852 158951: gap of 100 bp in length
* 158952 161241: contig of 2290 bp in length
* 161242 161341: gap of 100 bp in length
* 161342 163307: contig of 1966 bp in length
* 163308 163407: gap of 100 bp in length
* 163408 165487: contig of 2080 bp in length
* 165488 165587: gap of 100 bp in length
* 165588 167734: contig of 2147 bp in length
* 167735 167834: gap of 100 bp in length
* 167835 168855: contig of 1021 bp in length
* 168856 168955: gap of 100 bp in length
* 168956 170089: contig of 1134 bp in length
* 170090 170189: gap of 100 bp in length
* 170190 170655: contig of 466 bp in length
* 170656 170755: gap of 100 bp in length
* 170756 171980: contig of 1225 bp in length.

FEATURES
    source
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            /chromosome="11"
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            13699..26815
                /note="assembly-fragment"
            26916..37862
                /note="assembly-fragment"
            37963..46388
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            116902..121989
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            126047..132109
                /note="assembly-fragment"
            132210..136422
                /note="assembly-fragment"

Query Match      68.7%; Score 20.6; DB 2; Length 171980;
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Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagcaccacgtccgcatgcagatcc 30

Db 25058 GGCAGCACCATGTCCTCATGAGATCC 25032

RESULT 30

AP001558

LOCUS

DEFINITION Homo sapiens chromosome 11 clone RP11-686D5 map 11q13, WORKING

DRAFT SEQUENCE, 40 unordered pieces.

AP001558

AP001558.2 GI:8117392

VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS Homo sapiens DNA, clone:RP11-686D5.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 178100)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Home sapiens 178,100 genomic DNA of 11q13

Published Only in Database (2000) In press

2 (bases 1 to 178100)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Submitted (29-MAR-2000) Masahito Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,

Japan (E-mail:hattori@gsr.riken.go.jp

URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,

Fax:81-42-778-9924)

On May 30, 2000 this sequence version replaced gi:7380893.

----- Genome Center

Center: RIKEN Genomic Sciences Center(GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsr.riken.go.jp

----- Project Information

Center project name: RP11-686D5

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 148042 bases at least Q40

Consensus quality: 162125 bases at least Q30

Consensus quality: 169512 bases at least Q20

Insert size: 174200; sum-of-contigs

Quality coverage: 4.12x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of

40 contigs. The true order of the pieces is not known and their

order in this sequence record is arbitrary. Gaps between the

contigs are represented as runs N, but the exact sizes of the gaps

are unknown. This record will be updated with the finished sequence

as soon as it is available and the accession number will be

preserved

1 20070 contig of 20070 bp in length

20171 34749 contig of 14579 bp in length

34850 50049 contig of 15200 bp in length

50150 60765 contig of 10616 bp in length

60866 67727 contig of 6862 bp in length

67828 76362 contig of 8535 bp in length

76463 82230 contig of 5766 bp in length

82331 89521 contig of 7191 bp in length

89622 95129 contig of 5866 bp in length

95230 101095 contig of 5060 bp in length

101196 106255 contig of 4446 bp in length

106356 110801 contig of 4446 bp in length

110902 114837 contig of 3936 bp in length
114938 120430 contig of 5493 bp in length
120531 125238 contig of 4708 bp in length
125339 128370 contig of 3032 bp in length
128471 131184 contig of 2714 bp in length
131285 134627 contig of 3343 bp in length
134728 137446 contig of 2719 bp in length
137547 140281 contig of 2735 bp in length
140382 142601 contig of 2220 bp in length
142702 145477 contig of 2988 bp in length
145578 148565 contig of 2517 bp in length
148666 151182 contig of 2534 bp in length
151283 153836 contig of 2300 bp in length
153937 156236 contig of 1482 bp in length
156337 159802 contig of 1884 bp in length
157919 161284 contig of 1382 bp in length
159903 163110 contig of 1726 bp in length
161385 163211 contig of 1426 bp in length
163211 165594 contig of 1857 bp in length
164737 167968 contig of 1576 bp in length
167968 169543 contig of 1174 bp in length
169543 170824 contig of 1181 bp in length
170825 172804 contig of 1880 bp in length
172805 173997 contig of 1093 bp in length
174098 175750 contig of 1653 bp in length
175851 176984 contig of 1134 bp in length
176985 177085 contig of 1016 bp in length
177085 178100 contig of 1016 bp in length

Sequence updated (26-May-2006).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 20070: contig of 20070 bp in length
20071 20170: gap of 100 bp
20171 34749: contig of 14579 bp in length
34750 34849: gap of 100 bp
34850 50049: contig of 15200 bp in length
50050 50149: gap of 100 bp
50150 60765: contig of 10616 bp in length
60766 60865: gap of 100 bp
60866 67727: contig of 6862 bp in length
67728 67827: gap of 100 bp
67828 76362: contig of 8535 bp in length
76363 76462: gap of 100 bp
76463 82230: contig of 5768 bp in length
82231 82330: gap of 100 bp
82331 89521: contig of 7191 bp in length
89522 89621: gap of 100 bp
89622 95129: contig of 5508 bp in length
95130 95229: gap of 100 bp
95230 101095: contig of 5866 bp in length
101096 101195: gap of 100 bp
101196 106255: contig of 5060 bp in length
106256 106355: gap of 100 bp
106356 110801: contig of 4446 bp in length
110802 110901: gap of 100 bp
110902 114837: contig of 3936 bp in length
114838 114937: gap of 100 bp
114938 120430: contig of 5493 bp in length
120431 120530: gap of 100 bp
120531 125238: contig of 4708 bp in length
125239 125338: gap of 100 bp
125339 128370: contig of 3032 bp in length
128371 128470: gap of 100 bp
128471 131184: contig of 2714 bp in length
131185 131284: gap of 100 bp
131285 134627: contig of 3343 bp in length
134628 134727: gap of 100 bp

134728 137446: contig of 2719 bp in length
137447 137546: gap of 100 bp
137547 140281: contig of 2735 bp in length
140282 140381: gap of 100 bp
140382 142601: contig of 2220 bp in length
142602 142701: gap of 100 bp
142702 145477: contig of 2776 bp in length
145478 145577: gap of 100 bp
145578 148565: contig of 2988 bp in length
148566 148665: gap of 100 bp
148666 151182: contig of 2517 bp in length
151183 151282: gap of 100 bp
151283 153836: contig of 2534 bp in length
153837 153936: gap of 100 bp
153937 156236: contig of 2300 bp in length
156237 156336: gap of 100 bp
156337 157818: contig of 1482 bp in length
157819 157918: gap of 100 bp
157919 159802: contig of 1884 bp in length
159803 159902: gap of 100 bp
159903 161284: contig of 1382 bp in length
161285 161384: gap of 100 bp
161385 163110: contig of 1726 bp in length
163111 163210: gap of 100 bp
163211 164636: contig of 1426 bp in length
164637 164736: gap of 100 bp
164737 166593: contig of 1857 bp in length
166594 166693: gap of 100 bp
166694 167867: contig of 1174 bp in length
167868 167967: gap of 100 bp
167968 169543: contig of 1576 bp in length
169544 169643: gap of 100 bp
169644 170824: contig of 1181 bp in length
170825 170924: gap of 100 bp
170925 172804: contig of 1880 bp in length
172805 172904: gap of 100 bp
172905 173997: contig of 1093 bp in length
173998 174097: gap of 100 bp
174098 175750: contig of 1653 bp in length
175751 175850: gap of 100 bp
175851 176984: contig of 1134 bp in length
176985 177084: gap of 100 bp
177085 178100: contig of 1016 bp in length.

Location/Qualifiers

1. 178100
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="RP11-686D5"
1. 20070
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20171. 34749
/note="assembly_fragment"
34850. 50049
/note="assembly_fragment"
50150. 60765
/note="assembly_fragment"
60866. 67727
/note="assembly_fragment clone_end:77 vector_side:right"
67828. 76362
/note="assembly_fragment clone_end:SP6 vector_side:right"
76463. 82230
/note="assembly_fragment"

FEATURES

source

Query Match 68.7%; Score 20.6; DB 2; Length 178100;
Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggccagccacgaatccgatccgatcc 30
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Db 155737 GGCAGCACATGTCATCATGAGATCC 155763

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RESULT 31
AC090316 187483 bp DNA linear HTG 21-JUL-2001
DEFINITION Homo sapiens chromosome 11 clone RP11-772K10 map 11, WORKING DRAFT
ACCESSION AC090316
VERSION AC090316.2 GI:14971266
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187483)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-772K10
Unpublished
2 (bases 1 to 187483)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarta,J., Campoliano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRoque,K., Lamazares,R., Landers,T.,
Lehoczky,J., Levine,R., Liu,G., Maclean,C., MacDonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Menes,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhng,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sounez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Struss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zemek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 20, 2001 this sequence version replaced gi:12957952.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12585
Center clone name: 772.K10
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177293 bases at least Q40
Consensus quality: 181933 bases at least Q30
Consensus quality: 183738 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 185283; sum-of-ctnigs
Quality coverage: 6.3 in Q20 bases; sum-of-ctnigs
Quality coverage: 6.2 in Q20 bases; sum-of-ctnigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

```

```

* be preserved.
1
9135 9234: gap of 9134 bp in length
9235 10076: contig of 842 bp in length
10077 10176: gap of 100 bp
10177 11210: contig of 1034 bp in length
11211 11310: gap of 100 bp
11311 11521: contig of 211 bp in length
11522 11621: gap of 100 bp
11622 13944: contig of 2323 bp in length
13945 14044: gap of 100 bp
14045 16117: contig of 2073 bp in length
16118 16217: gap of 100 bp
16218 35961: contig of 19744 bp in length
35962 36061: gap of 100 bp
36062 38758: contig of 2697 bp in length
38759 38858: gap of 100 bp
38859 42149: contig of 3291 bp in length
42150 42249: gap of 100 bp
42250 46505: contig of 4256 bp in length
46506 46605: gap of 100 bp
46606 51462: contig of 4857 bp in length
51463 51562: gap of 100 bp
51563 57004: contig of 5442 bp in length
57005 57104: gap of 100 bp
57105 64258: contig of 7154 bp in length
64259 64358: gap of 100 bp
64359 69102: contig of 4744 bp in length
69103 69202: gap of 100 bp
69203 80578: contig of 11376 bp in length
80579 80678: gap of 100 bp
80679 91084: contig of 10406 bp in length
91085 91184: gap of 100 bp
91185 99902: contig of 8718 bp in length
99903 100002: gap of 100 bp
100003 114020: contig of 14018 bp in length
114021 114120: gap of 100 bp
114121 128914: contig of 14794 bp in length
128915 129014: gap of 100 bp
129015 140836: contig of 11822 bp in length
140837 140936: gap of 100 bp
140937 162541: contig of 21605 bp in length
162542 162641: gap of 100 bp
162642 185670: contig of 23029 bp in length
185671 185770: gap of 100 bp
185771 187483: contig of 1713 bp in length.
location/Qualifiers
1. 187483
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-772K10"
/clone_lib="RPC1-11 Human Male BAC"
1. 9134
/note="assembly-fragment"
clone_end:SP6
vector_side:left"
9235. 10076
/note="assembly-fragment"
10177. 11210
/note="assembly-fragment"
11311. 11521
/note="assembly-fragment"
11622. 13944
/note="assembly-fragment"
14045. 16117
/note="assembly-fragment"
16218. 35961
/note="assembly-fragment"
36062. 38758
/note="assembly-fragment"
38859. 42149

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misc_feature      /clone="RP11-686D5"
                  /clone_lib="RPC1-11 Human Male BAC"
                  1..21293
                  /note="assembly_fragment"
misc_feature      /note="assembly_side:left"
                  clone_end:SP6
                  vector_side:left"
                  21394..22583
                  /note="assembly_fragment"
misc_feature      22684..23723
                  /note="assembly_fragment"
misc_feature      23824..25980
                  /note="assembly_fragment"
misc_feature      26081..67365
                  /note="assembly_fragment"
misc_feature      67466..70288
                  /note="assembly_fragment"
misc_feature      70389..81723
                  /note="assembly_fragment"
misc_feature      81824..93377
                  /note="assembly_fragment"
misc_feature      93478..125021
                  /note="assembly_fragment"
misc_feature      125122..156983
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misc_feature      157084..198328
                  /note="assembly_fragment"
misc_feature      198429..200026
                  /note="assembly_fragment"
                  clone_end:T7
                  vector_side:right"
BASE COUNT      45868 a 55290 c 53297 g 44469 t 1102 others
ORIGIN
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Query Match      68.7% Score 20.6; DB 2; Length 200026;
Best Local Similarity 85.2% Pred. No.2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      4 ggcagcaccgaagtcgcgatcgatcc 30
          ||||| ||||| ||||| ||||| |||||
Db 169453 GGCAGCACCATGTCCTCATCGATGCC 169479
```

```
RESULT 33
AC004076      41322 bp DNA linear PRI 29-JAN-1998
LOCUS      Homo sapiens chromosome 19, cosmid R30217, complete sequence.
DEFINITION
AC004076      AC004076.1 GI:2822142
VERSION
KEYWORDS      HTG.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 41322)
AUTHORS      Lamerdin,J.E., McCreedy,P.M., Skowronski,E., Adamson,A.W.,
                Burkhart-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stillwegen,S.,
                Gaines,J., Dangnan,L., Poundstone,P., Christensen,M.,
                Georgescu,A., Avila,J., Liu,S., Bruce,R., Quan,G., Montgomery,M.,
                Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.O. and
                Carrano,A.V.
TITLE      Sequence analysis of a 500 kb ZNF gene family- containing human
                contig in 19q13.4
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 41322)
AUTHORS      Lamerdin,J.E.
TITLE      Direct Submission
JOURNAL      Submitted (29-JAN-1998) Joint Genome Institute, Lawrence Livermore
                National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
COMMENT      Map and sequence oriented from centromere to q telomere.
                Cosmid R30217 overlaps cosmid R28253 to the left and F18750 to the
                right.
```

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FEATURES
source
location/Qualifiers
1..41322
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.4 between D19S303 and ZNF134"
/clone="R30217"
/cell_line="5H12-B"
/clone_lib="L119NC032 R chromosome 19-specific cosmid"
/note="cosmid library constructed at LNL, from flow-sorted
chromosomes from hybrid 5H12-B, which carries chromosome
19 as its only human chromosome."
1..1431
/note="BLASTN similarity to AC003002 (80114..81544);
match: 1, score: 1.8e-294; database searched: nt; Human
DNA from overlapping chromosome 19-specific cosmids R29515
and R28253, genomic sequence, complete sequence [Homo
sapiens]"
complement(10..98)
/rpt_family="MSTC"
383..680
/rpt_family="AluSc"
complement(989..1286)
/note="TDS similarity to AA229025 nc50c11.s1 NCI CGAP_Pt3
Homo sapiens CDNA clone IMAGE:1011572. Score: 550
identity: 290/300 (96%)."
1281..1318
/rpt_family="POIX-A"
complement(1443..1755)
/rpt_family="AluSp"
1917..2204
/rpt_family="AluSx"
complement(2735..2777)
/rpt_family="(CA)n"
3566..3652
/rpt_family="FRAM/FAM"
3671..3719
/rpt_family="MERAD"
complement(3720..4019)
/rpt_family="AluSp"
4047..4324
/rpt_family="MERAD"
4960..5217
/note="TDS similarity to multiple ESTs:
(4960..5217) AA446441 zw60d10.r1 Soares total fetus Nb2HF8
9w Homo sapiens CDNA clone 774451 5' similar to contains
LTR3.t2 LTR3 repetitive element ;
(1..259): 98% identity~(4962..5216) AA195132 zr34b08.r1
Soares NhMPu S1 Homo sapiens CDNA clone 665271 5' similar
to contains LTR3.b1 LTR3 repetitive element; (1..253): 99%
identity~(4962..5216) W03459 za06e09.r1 Soares melanocyte
2NDHf Homo sapiens CDNA clone 291784 5' similar to
contains LTR3.b1 LTR3 repetitive element;(1..253): 96%
identity.
and others."
complement(5599..5875)
/rpt_family="LINE2"
complement(6952..6980)
/rpt_family="AT-rich"
7067..7364
/rpt_family="AluSg"
complement(7488..7593)
/rpt_family="MIR"
7718..8134
/rpt_family="LTR3"
complement(8649..9102)
/rpt_family="LINE2"
9114..9386
/rpt_family="AluJo"
9573..9676
/note="predicted exon, program: gfall2exons_human_1.3,
frame: 1, quality: excellent, score: 90.000"
10469..10758
repeat_region
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repeat_region /rpt_family="AluSg"
11041..11377
/rpt_family="MER74"
misc_feature 11448..11576
/Note="DPS similarity to (U66561) kruppel-related zinc
finger protein [Homo sapiens] (1..43); 48% identity. -Other
overlapping matches:
(11508..11634) predicted exon, program:
grail2exons_human_1.3, frame: 2, quality: excellent,
score: 83.000"
12108..12167
/Note="DPS similarity to (U66561) kruppel-related zinc
finger protein [Homo sapiens] (45..63); 26% identity.

misc_feature 12861..12900
/rpt_family="MER4D"
12973..13537
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finger protein [Homo sapiens] (64..243). -Other overlapping
matches:
(12973..15108) predicted exon, program:
grail2exons_human_1.3, frame: 0, quality: excellent,
score: 87.000"
13033..15108
/Note="hypothetical ZNF-like protein"
/codon_start=1
/product="R30217_1"
/protein_id="AAB97932.1"
/db_xref="GI:2822143"
/translation="MCSSTLKDLILHAEDGTHPPQGLYTCAEHDLHOKEDIREKLT
RSDMRPSTVNSAHVGERNFTCTGGKDFIASDILQOQVINSGLKLYRDYDEAF
OGEQNDPNSQGGKDFCHQHGLEHOKTHNGRPYEFSEGLFRNSMLIYQONHA
GERPYEGTEYKFTIRKSNLYOHOKIHSGFLSKSDPIEHEDILSRPYECCTCGK
AFLTALHVGHQKTHTEQPYECNKGKFFNYSKLIHQKVTGERRECEGCGFLF
MDSFTLGRHORVHTGERPECSICGSEFHSRSTLNMHGVHGRKLYKCEGSKAFSL
KHNVOHLKIHTEGRRPYECTCEKAFVRSKHLYOHOKITTHDAKRSRSDIQKRI DIR
PRPYCEGSKAFILOAHVGHOKIHTGRRPYECTOCAAAFYRKSHLVQHEKIHIDAF
SKRSDIQKRIIDLKRPYVCEGNAFLTOHLQGHOKIQGERRECEGCGKFFLD
SKYLVHQRHTEGRRPYECNKGKFFRYSCTLSRQKVTGERRECEGCGKFFLD
KLIHQVHTGERPYECNKGKFLRYRSTFIHNNVCTGEKDECSKCELPRTSSSL
LIHQSHTEGSPFLRECGKDFNKCNTGQRQKTHNGERSYECGESSKVKYNSLIKH
OIIHNGRP"
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finger protein [Homo sapiens] (250..417).
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/Note="DPS similarity to (U66561) kruppel-related zinc
finger protein [Homo sapiens] (418..473).
"
misc_feature 14366..15116
/Note="DPS similarity to (U66561) kruppel-related zinc
finger protein [Homo sapiens] (474..726).
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repeat_region /rpt_family="AluSx"
15272..15565
complement(15566..15720)
/rpt_family="L1MB3"
15721..16037
/rpt_family="MER1B"
repeat_region /rpt_family="L1MB3"
16037..16255
complement(16055..16255)
/rpt_family="L1MB3"
16256..17064
/rpt_family="MER7B"
repeat_region /rpt_family="AluSg"
17065..17363
complement(17065..17363)
/rpt_family="AluSg"
17364..17658
complement(17364..17658)
/rpt_family="AluSg"
17659..17849
/rpt_family="MER7B"
repeat_region /rpt_family="L1MB3"
18015..18050
complement(18051..18348)
/rpt_family="L1MB3"
repeat_region /rpt_family="L1MB3"
18051..18348
complement(18051..18348)

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complement(18358..19222)
/rpt_family="L1MB3"
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(98%).
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repeat_region /rpt_family="POLY_A"
complement(20832..20969)
/rpt_family="MSTC"
repeat_region /rpt_family="AluSp"
complement(21068..21397)
/rpt_family="AluSp"
repeat_region /rpt_family="MSTC"
complement(21402..21590)
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21846..22198
/rpt_family="MSTC"
repeat_region /rpt_family="MSTC"
complement(22532..22641)
/rpt_family="L1MB9"
repeat_region /rpt_family="L1MB9"
complement(22738..22856)
/rpt_family="CGAA)n"
repeat_region /rpt_family="CGAA)n"
complement(22871..23168)
/rpt_family="AluSp"
repeat_region /rpt_family="AluSp"
complement(23254..23400)
/rpt_family="L1MB"
repeat_region /rpt_family="L1MB"
complement(23450..23642)

Query Match 68.0% Score 20.4; DB 9; Length 41322;
Best Local Similarity 80.0% Pred. No. 3.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ctggcagcaccacgagtcgagtcgagtcacatcc 30
|||||
Db 36452 CTGGCAGACACAGCGTTCCATGCACACTCC 36481

RESULT 34
AC005807 65870 bp DNA linear ROD 01-DEC-1998
LOCUS Mus musculus chromosome 17 BAC clone c1b585c7 from MHC region,
DEFINITION complete sequence.
ACCESSION AC005807
VERSION AC005807.1 GI:3935210
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65870)
REFERENCE Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Butler,C., Card,P., desailboat,C., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gordon,M., Grant,O.,
Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N., Major,T.,
McFarland,J., Newton,J., Osborne-Lawrence,S., Schageman,J.,
Schultz,R.A., Stimson,S., Wagner,N., Waller,K. and Ward,T.
HTGS Submission
Unpublished
2 (bases 1 to 65870)
Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Butler,C., Card,P., desailboat,C., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gordon,M., Grant,O.,
Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N., Major,T.,
McFarland,J., Newton,J., Osborne-Lawrence,S., Schageman,J.,
Schultz,R.A., Stimson,S., Wagner,N., Waller,K. and Ward,T.
Direct Submission
Submitted (10-OCT-1998) Genome Science & Technology Center,
University of Texas Southwestern Medical Center, 5323 Harry Hines
Blvd, Dallas, TX 75235-8591, USA
3 (bases 1 to 65870)
Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Butler,C., Card,P., desailboat,C., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,

```



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* 124307 127520: contig of 3214 bp in length
* 127521 127620: gap of unknown length
* 127621 131710: contig of 4090 bp in length
* 131711 131810: gap of unknown length
* 131811 135916: contig of 4106 bp in length
* 135917 136016: gap of unknown length
* 136017 138794: contig of 2778 bp in length
* 138795 138894: gap of unknown length
* 138895 144037: contig of 5143 bp in length
* 144038 144137: gap of unknown length
* 144138 146347: contig of 2210 bp in length
* 146348 146447: gap of unknown length
* 146448 150379: contig of 3932 bp in length
* 150380 150479: gap of unknown length
* 150480 154510: contig of 4031 bp in length
* 154511 154610: gap of unknown length
* 154611 157925: contig of 3315 bp in length
* 157926 158025: gap of unknown length
* 158026 160712: contig of 2687 bp in length
* 160713 160812: gap of unknown length
* 160813 163479: contig of 2667 bp in length
* 163480 163579: gap of unknown length
* 163580 165744: contig of 2165 bp in length
* 165745 165844: gap of unknown length
* 165845 168563: contig of 2719 bp in length.
Location/Qualifiers
1. 168563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3p"
/clone="RP11-474M18"

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BASE COUNT 51285 a 30469 c 30057 g 54000 t 2752 others
ORIGIN

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Query Match 67.3% Score 20.2; DB 2; Length 168563;
Best Local Similarity 88.0% Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

Oy 6 cagcaccagtcgcgatccagatcc 30
||||||| ||| |||||||||
Db 114893 CAGCACCAATCCACATCGCATCC 114917

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RESULT 36
AC023547 178415 bp DNA linear HTG 26-MAY-2000
LOCUS Homo sapiens chromosome 1 clone RP11-474M18 map 1, WORKING DRAFT
DEFINITION AC023547
SEQUENCE, 12 unordered pieces.
AC023547
AC023547.3 GI:8076834
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178415)
Birten,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 1, clone RP11-474M18
Unpublished
2 (bases 1 to 178415)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhgelter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferrelia,P., Fitzhugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., Mcpheeters,R., Meldrum,J.,

```

TITLE JOURNAL COMMENT

Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced g1:7331465.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information -----
Center project name: 16353
Center clone name: 474_M18

----- Summary Statistics -----
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 171351 bases at least Q40
Consensus quality: 174924 bases at least Q20
Consensus quality: 176088 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 177315; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 5.1 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 1 1730: contig of 1730 bp in length
* 1731 1830: gap of 100 bp
* 1831 4407: contig of 2577 bp in length
* 4408 4507: gap of 100 bp
* 4508 9349: contig of 4842 bp in length
* 9350 9449: gap of 100 bp
* 9450 15955: contig of 6506 bp in length
* 15956 16055: gap of 100 bp
* 16056 20307: contig of 4252 bp in length
* 20308 20407: gap of 100 bp
* 20408 26374: contig of 5967 bp in length
* 26375 26474: gap of 100 bp
* 26475 39624: contig of 13150 bp in length
* 39625 39724: gap of 100 bp
* 39725 57149: contig of 17425 bp in length
* 57150 57249: gap of 100 bp
* 57250 76223: contig of 18974 bp in length
* 76224 76323: gap of 100 bp
* 76324 101233: contig of 24910 bp in length
* 101234 101333: gap of 100 bp
* 101334 132080: contig of 30747 bp in length
* 132081 132180: gap of 100 bp
* 132181 178415: contig of 46235 bp in length.
Location/Qualifiers
1. 178415
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1"

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FEATURES source

/clone_lib="RP11-474M18"
misc_feature 1..1730 /note="assembly-fragment"
misc_feature 1831..4407 /note="assembly-fragment"
misc_feature 4508..9349 /note="assembly-fragment"
misc_feature 9450..15955 /note="assembly-fragment"
misc_feature 16056..20307 /note="assembly-fragment"
misc_feature 20408..26374 /note="assembly-fragment"
misc_feature 26475..39624 /note="assembly-fragment"
misc_feature 39725..57149 /note="assembly-fragment"
misc_feature 57250..76223 /note="assembly-fragment"
misc_feature 76324..101233 /note="assembly-fragment"
misc_feature 101334..132080 /note="assembly-fragment"
misc_feature 132181..178415 /note="assembly-fragment"
BASE COUNT 60179 a 31444 c 30146 g 55546 t 1100 others
ORIGIN

Query Match 67.3% Score 20.2; DB 2; Length 178415;
Best Local Similarity 88.0%; Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 cagcaccgaagtcggatcgagatcc 30
|||||
DB 113773 CAGCACCAATCCACATCGCATGCC 113797

RESULT 37
AB01082S01/c 3194 bp DNA linear PRI 14-APR-2000
LOCUS Homo sapiens MASP gene for mannose binding protein-associated
DEFINITION protease, exon 1.
ACCESSION AB010822
VERSION AB010822.1 GI:3985963
KEYWORDS MASP; mannose binding protein-associated protease.
SEGMENT 1 of 16
SOURCE Homo sapiens DNA, clone_lib:lamda FIX II clone:F419.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Endo, Y.
TITLE Molecular evolution of mannose binding protein-associated serine
protease (MASP)
JOURNAL Unpublished (1998)
REFERENCE 2 (bases 1 to 3194)
AUTHORS Endo, Y.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1998) Yuichi Endo, Fukushima Medical College,
Dept. of Biochemistry; 1-Hikarigaoka, Fukushima-shi, Fukushima
960-12, Japan (E-mail: yendo@cc.fmu.ac.jp, Tel: 81-245-48-2111,
Fax: 81-245-48-6760)
FEATURES
source Location/Qualifiers
1..3194 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="F419"

5'UTR /clone_lib="lamda FIX II"
2379..2428
/gene="MASP"
exon 2379..2433
/gene="MASP"
/number=1
BASE COUNT 877 a 696 c 733 g 888 t
/product="mannose binding protein-associated protease"
ORIGIN

Query Match 66.7% Score 20; DB 9; Length 3194;
Best Local Similarity 82.1%; Pred. No. 5.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctggcagcaccgaagtcggatcgagatc 28
|||||
DB 1694 CTGGGAGCACCACCAAGTCGTGATGGCT 1667

RESULT 38
COTLEOC 4943 bp DNA linear PLN 31-MAY-1994
LOCUS Gossypium hirsutum 18.2 kDa oleosin (Matp6-A) gene, complete cds.
DEFINITION L00936
ACCESSION L00936
VERSION L00936.1 GI:167364
KEYWORDS 18.2 kDa oleosin; membrane protein.
SOURCE Gossypium hirsutum (strain Coker 201) DNA.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 4943)
AUTHORS Hughes, D.W., Wang, H.Y. and Galau, G.A.
Cotton (Gossypium hirsutum) Matp6 and Matp7 oleosin genes
JOURNAL Plant Physiol. 101, 697-698 (1993)
MEDLINE 94105311

FEATURES
source Location/Qualifiers
1..4943 /organism="Gossypium hirsutum"
/strain="Coker 201"
/db_xref="taxon:3635"
/dev_stage="embryos, 20-23 days postanthesis
(preendoreduplication) cotyledon"

5'UTR /gene="Matp6-A"
3265..3348 /note="putative"
gene 3265..4067 /gene="Matp6-A"
3265..4067 /note="putative"
mRNA 3265..4067 /gene="Matp6-A"
/evidence="experimental"
CDS 3349..3855 /gene="Matp6-A"
/note="putative"
/citation=[1]
/codon_start=1
/product="18.2 kDa oleosin"
/protein_id="AA18525.1"
/db_xref="GI:167365"
/translation="MAVYRDRNLPHQYVHPQYRDLNNTGGCGYAKNYSRSTSOVL
AVLLPLPTGGTLLAGLLTACTVIGMLATPDLFTTFSPVLPALAIAMATGFLSS
GAFGLTGLSSLYVINRLRYATGTBOLDLDAKRRVODMTEYVGKTEYVGKLENNKA
HEGQVGR"
3856..4067 /gene="Matp6-A"
/note="putative"
4042..4047 /gene="Matp6-A"
/note="putative"
4067 /gene="Matp6-A"
/evidence="experimental"

BASE COUNT	1687 a	750 c	790 g	1716 t	
ORIGIN					
Query Match	66.7%	Score 20:	DB 8:	Length 4943;	
Best Local Similarity	82.1%;	Pred. No. 5.3e+02;			
Matches	23:	Conservative	0:	Mismatches 5; Indels 0; Gaps 0;	
Oy	2	tgggcagcaccgaatcgccgagtcgacgac	29		
Db	236	TAGCGCAGCATTCAGTCGACATGCATGC	263		
RESULT 39					
LOCUS	AC097195				
DEFINITION	AC097195	275272 bp	DNA	linear HTG 20-DEC-2001	
ACCESSION	AC097195				
VERSION	AC097195.4	GI:17973587			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 275272)				
AUTHORS	Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barbarta,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Butch,P., Burkelt,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gall,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homs,I.F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Loliseged,L., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Matlindale,A., Matlizee,E., Massey,E., Mawhney,E., Mcleod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwouon,G., Otagunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Peters,L., Pickens,R., Primus,E., Pu,L., L., Ruitz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtrali,N., Slason,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stoson,H., Sutton,A., Swatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.				
TITLE	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 275272)				
AUTHORS	Worley,K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-OCT-2001)				

COMMENT

```

Baylor Plaza, Houston, TX 77030 USA
On Dec 20, 2001 this sequence version replaced gi:17064469.

----- Genome Center -----

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: G1CS
Center clone name: CH230-190H11
Summary Statistics

Assembly program: Phrap; version 0.990329First call to
findHreplist

Consensus quality: 255286 bases at least Q40
Consensus quality: 265116 bases at least Q30
Consensus quality: 273271 bases at least Q20
Estimated insert size: 252419; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-tp estimation
Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation

-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 44260: contig of 44260 bp in length
44261 44360: gap of unknown length
44361 68945: contig of 24585 bp in length
68946 69045: gap of unknown length
69046 86655: contig of 17620 bp in length
86656 86765: gap of unknown length
86766 101226: contig of 14461 bp in length
101227 101326: gap of unknown length
101327 114853: contig of 13527 bp in length
114854 114953: gap of unknown length
114954 128069: contig of 13116 bp in length
128070 128169: gap of unknown length
128170 137924: contig of 9755 bp in length
137925 138024: gap of unknown length
138025 147475: contig of 9451 bp in length
147476 147575: gap of unknown length
147576 156000: contig of 8425 bp in length
156001 156100: gap of unknown length
156101 162216: contig of 6116 bp in length
162217 162316: gap of unknown length
162317 167453: contig of 5136 bp in length
167454 167552: gap of unknown length
167553 173652: contig of 6100 bp in length
173653 173752: gap of unknown length
173753 177557: contig of 3805 bp in length
177558 177657: gap of unknown length
177659 181671: contig of 4014 bp in length
181672 181772: gap of unknown length
181773 186032: contig of 4261 bp in length
186033 186132: gap of unknown length
186133 190078: contig of 3446 bp in length
190079 190178: gap of unknown length
190179 194272: contig of 4094 bp in length
194273 194372: gap of unknown length
194373 198004: contig of 3632 bp in length
198005 198104: gap of unknown length
198105 201600: contig of 3496 bp in length
201601 201700: gap of unknown length
201701 204721: contig of 3021 bp in length
204722 204821: gap of unknown length
204822 207829: contig of 3008 bp in length
207830 207929: gap of unknown length

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207930	*	210021	contig of 2092	bp in length
210022	*	210121	gap of unknown	length
210122	*	212766	contig of 2645	bp in length
212867	*	212866	gap of unknown	length
212867	*	215930	contig of 3064	bp in length
215931	*	216030	gap of unknown	length
216031	*	218057	contig of 2027	bp in length
218058	*	218157	gap of unknown	length
218158	*	219598	contig of 1441	bp in length
219599	*	219698	gap of unknown	length
219699	*	222618	contig of 2920	bp in length
222619	*	222718	gap of unknown	length
222719	*	225859	contig of 3141	bp in length
225860	*	225959	gap of unknown	length
225960	*	227832	contig of 1873	bp in length
227833	*	227933	gap of unknown	length
227933	*	230488	contig of 2556	bp in length
230489	*	230588	gap of unknown	length
230589	*	232812	contig of 2324	bp in length
232913	*	233012	gap of unknown	length
233013	*	234385	contig of 1373	bp in length
234386	*	234485	gap of unknown	length
234486	*	235883	contig of 1398	bp in length
235884	*	235983	gap of unknown	length
235984	*	237590	contig of 1607	bp in length
237591	*	237690	gap of unknown	length
237691	*	239482	contig of 1792	bp in length
239483	*	239582	gap of unknown	length
239583	*	241021	contig of 1439	bp in length
241022	*	241121	gap of unknown	length
241122	*	243601	contig of 2460	bp in length
243602	*	243701	gap of unknown	length
243702	*	245107	contig of 1406	bp in length
245108	*	245207	gap of unknown	length
245208	*	246935	contig of 1728	bp in length
246936	*	247035	gap of unknown	length
247036	*	248780	contig of 1745	bp in length
248781	*	248880	gap of unknown	length
248881	*	250984	contig of 2104	bp in length
250985	*	251084	gap of unknown	length
251085	*	252683	contig of 1599	bp in length
252684	*	252783	gap of unknown	length
252784	*	253688	contig of 1085	bp in length
253689	*	253968	gap of unknown	length
253969	*	255016	contig of 1048	bp in length
255017	*	255116	gap of unknown	length
255117	*	256306	contig of 1190	bp in length
256307	*	256406	gap of unknown	length
256407	*	258016	contig of 1610	bp in length
258017	*	258116	gap of unknown	length
258117	*	259924	contig of 1808	bp in length
259925	*	260024	gap of unknown	length
260025	*	261112	contig of 1088	bp in length
261113	*	261212	gap of unknown	length
261213	*	263047	contig of 1835	bp in length
263048	*	263147	gap of unknown	length
263148	*	264800	contig of 1653	bp in length
264801	*	264900	gap of unknown	length
264901	*	266364	contig of 1464	bp in length
266365	*	266464	gap of unknown	length
266465	*	267855	contig of 1391	bp in length
267856	*	267955	gap of unknown	length
267956	*	269294	contig of 1339	bp in length
269295	*	269394	gap of unknown	length
269395	*	270960	contig of 1566	bp in length
270961	*	271060	gap of unknown	length
271061	*	272125	contig of 1065	bp in length
272126	*	272225	gap of unknown	length
272226	*	273587	contig of 1362	bp in length

Oy	1	ctgggcagcaccagaatccgcatgcacgat	28
Db	168077	CGGGGCACGCAAAAAGTCCGATGACGAT	168104
RESULT	40		
LOCUS	HS157D1LR		
DEFINITION	H.sapiens Cpg island DNA genomic MseI fragment, clone 157d1l,	DNA	PRI 19-Oct-1995
ACCESSION	Z59486		
VERSION	259486.1	GI:1031399	
KEYWORDS	Cpg island; genomic MseI fragment.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 258)		
JOURNAL	Dodsworth,S.J., Huckle,E., Wilkinson,P. and Micklem,G. Direct Submission Submitted (16-Oct-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk		
REFERENCE	2 (bases 1 to 258) Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P. Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)		
AUTHORS	94282070		
TITLE	Vector: pGEM-5zf(-)		
JOURNAL	Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.homp.mrc.ac.uk/ for details or contact: biohelp@hmp.mrc.ac.uk.		
MEDLINE	Location/Qualifiers		
FEATURES	1..258		
source	/organism="Homo sapiens" /db_xref="taxon:9606" /sex="male" /dex_stage="adult" /tissue_type="blood" /clone_id="CGI-1" /clone="157d1l"		
BASE COUNT	41 a 69 c 91 g 55 t 2 others		
ORIGIN			
Query Match	65.3%; Score 19.6; DB 9; Length 258; Best Local Similarity 84.6%; Pred. No. 8.2e+02; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Oy	1	ctgggcagcaccagaatccgcatgcacg	26
Db	67	CTGGGCACGACCACCAAGCGCGGTGCAG	92
RESULT	41		
LOCUS	AF254143		
DEFINITION	AF254143 5883 bp DNA linear PLN 21-SEP-2000		
ACCESSION	Candida albicans repressed by TUP1 protein 2 (RBZ) gene, complete cds.		
VERSION	AF254143		
KEYWORDS	AF254143.1 GI:9963983		
SOURCE	.		
ORGANISM	Candida albicans.		
REFERENCE	Candida albicans Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. 1 (bases 1 to 5883) Braun,B.R. and Johnson,A.D. TUP1, CPB1 and EFG1 make independent contributions to filamentation in candida albicans Genetics 155 (1), 57-67 (2000)		
JOURNAL	Genetics 155 (1), 57-67 (2000)		
MEDLINE	20253093		

* 10641 10740: gap of 100 bp
* 10741 11468: contig of 728 bp in length
* 11469 11568: gap of 100 bp
* 11569 12302: contig of 734 bp in length
* 12303 12402: gap of 100 bp
* 12403 13148: contig of 746 bp in length
* 13149 13248: gap of 100 bp
* 13249 13998: contig of 750 bp in length
* 13999 14098: gap of 100 bp
* 14099 14817: contig of 719 bp in length
* 14818 14917: gap of 100 bp
* 14918 15614: contig of 697 bp in length
* 15615 15714: gap of 100 bp
* 15715 16427: contig of 713 bp in length
* 16428 16527: gap of 100 bp
* 16528 17250: contig of 723 bp in length
* 17251 17350: gap of 100 bp
* 17351 18076: contig of 726 bp in length
* 18077 18176: gap of 100 bp
* 18177 18898: contig of 722 bp in length
* 18899 18998: gap of 100 bp
* 18999 19731: contig of 733 bp in length
* 19732 19831: gap of 100 bp
* 19832 20560: contig of 729 bp in length
* 20561 20660: gap of 100 bp
* 20661 21390: contig of 730 bp in length
* 21391 21490: gap of 100 bp
* 21491 22218: contig of 728 bp in length
* 22219 22318: gap of 100 bp
* 22319 23019: contig of 701 bp in length
* 23020 23119: gap of 100 bp
* 23120 23836: contig of 717 bp in length
* 23837 23936: gap of 100 bp
* 23937 24657: contig of 721 bp in length
* 24658 24757: gap of 100 bp
* 24758 25449: contig of 692 bp in length
* 25450 25549: gap of 100 bp
* 25550 26283: contig of 734 bp in length
* 26284 26383: gap of 100 bp
* 26384 27081: contig of 698 bp in length
* 27082 27181: gap of 100 bp
* 27182 27907: contig of 726 bp in length
* 27908 28007: gap of 100 bp
* 28008 28742: contig of 735 bp in length
* 28743 28842: gap of 100 bp
* 28843 29579: contig of 737 bp in length
* 29580 29679: gap of 100 bp
* 29680 30417: contig of 738 bp in length
* 30418 30517: gap of 100 bp
* 30518 31233: contig of 716 bp in length
* 31234 31333: gap of 100 bp
* 31334 32052: contig of 719 bp in length
* 32053 32152: gap of 100 bp
* 32153 32874: contig of 722 bp in length
* 32875 32974: gap of 100 bp
* 32975 33697: contig of 723 bp in length
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* 33798 34529: contig of 732 bp in length
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* 34630 35356: contig of 727 bp in length
* 35357 35456: gap of 100 bp
* 35457 36177: contig of 721 bp in length
* 36178 36277: gap of 100 bp
* 36278 37004: contig of 727 bp in length
* 37005 37104: gap of 100 bp
* 37105 37834: contig of 730 bp in length
* 37835 37934: gap of 100 bp
* 37935 38664: contig of 730 bp in length
* 38665 38764: gap of 100 bp
* 38765 39476: contig of 712 bp in length
* 39477 39576: gap of 100 bp
* 39577 40296: contig of 720 bp in length
* 40297 40396: gap of 100 bp

* 40397 41125: contig of 729 bp in length
* 41126 41225: gap of 100 bp
* 41226 41948: contig of 723 bp in length
* 41949 42048: gap of 100 bp
* 42049 42784: contig of 736 bp in length
* 42785 42884: gap of 100 bp
* 42885 43613: contig of 729 bp in length
* 43614 43713: gap of 100 bp
* 43714 44436: contig of 723 bp in length
* 44437 44536: gap of 100 bp
* 44537 45266: contig of 730 bp in length
* 45267 45366: gap of 100 bp
* 45367 46094: contig of 728 bp in length
* 46095 46194: gap of 100 bp
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* 46899 46998: gap of 100 bp
* 46999 47747: contig of 749 bp in length
* 47748 47847: gap of 100 bp
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* 48681 48399: contig of 719 bp in length
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* 52763 53490: contig of 728 bp in length
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* 53591 54326: contig of 736 bp in length
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* 54427 55128: contig of 702 bp in length
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Best Local Similarity 84.6%: Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 tgggcagcaccacgaatccgagtcagaga 27
Db 48464 TGGGAGCATCATGTCCAGATGCAGA 48439

RESULT 43
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LOCUS AC008956 110129 bp DNA linear PRI 21-JUL-2001
DEFINITION Homo sapiens chromosome 16 clone CTD-2343L5, complete sequence.
ACCESSION AC008956
VERSION AC008956.8 GI:14993669
KEYWORDS HMG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 110129)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 110129)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 110129)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell

REFERENCE 4 (bases 1 to 110129)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jul 21, 2001 this sequence version replaced gi:14572122.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.1.
 STS Content:
 SHGC-32146 G27136
 SHGC-60517 G36854.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="CTD-2343L5"
 BASE COUNT 28150 a 27910 c 27617 g 26452 t
 ORIGIN

Query Match 65.3%; Score 19.6; DB 9; Length 110129;
 Best Local Similarity 84.6%; Pred. No. 7.6e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagcaccagtcgcgagtcagatc 29
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 Db 2122 GGCAGCACCAAGCCGCGTGAGAGCTC 2147

RESULT 44
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 DEFINITION sequence.
 ACCESSION AC002544
 VERSION AC002544.1 GI:3337382
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 156641)
 Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
 Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q

TITLE
 JOURNAL Genomics 60 (3), 295-308 (1999)
 MEDLINE 99425270
 PUBMED 10493829

REFERENCE 2 (bases 1 to 156641)
 AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
 TITLE Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5
 JOURNAL Unpublished
 3 (bases 1 to 156641)
 Adams,M.D. and Loftus,B.J.
 TITLE Direct Submission
 JOURNAL Submitted (12-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, Email: mdadam@tigr.org
 4 (bases 1 to 156641)
 Adams,M.D. and Loftus,B.J.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

COMMENT
 On Jul 24, 1998 this sequence version replaced gi:2959563.
 Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgenet@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRail (available by anonymous ftp from arthur.epm.ornl.gov), Genetinder (Phil Green, University of Washington), Genscan (Chris Burge, http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the complete sequence against a peptide database, and the Human gene Index database at tigr (http://www.tigr.org/tdb/hgi/hgi.html).
 Genes without peptide homology having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAScan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAScan-SE/).
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 /chromosome="16"
 /map="16p11.2"
 /clone="A-761H5"
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 /db_xref="dbSTS:G30050"
 27016..108426
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 27383..27567
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STS
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VNSESEAKEEKEEESGTCWKLPFRQAGMSVRDPQQLPPVCKPLAPFQKTKID
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HRHSSGLPYWYLTAEKLRNMGROBPPOQSIINDNSLSLKTPECCITLPPSPVD
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139593. .139665,140471. .140556,140677. .140756,
141606. .141677,142305. .142401,144492. .144570,
144724. .144946))
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/complement(<130544. .144946)
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BASE COUNT 41602 a 38891 c 38211 g 37878 t 59 others
ORIGIN
Query Match 65.3%; Score 19.6; DB 9; Length 156641;
Best Local Similarity 84.6%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ggcagcaccaagtcggatgcagatc 29
Db 66730 GGCAGCACCAAGCCCGGATGGAGCTC 66755
RESULT 45
AC068137 166719 bp DNA linear PRI 09-JAN-2002
LOCUS AC068137
DEFINITION Homo sapiens BAC clone RP11-803A13 from 2, complete sequence.
AC068137
AC068137.8 GI:15375223
VERSION
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 166719)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 166719)
AUTHORS Du,H. and Doebber,A.
TITLE The sequence of Homo sapiens BAC clone RP11-803A13
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 166719)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 166719)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 166719)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 166719)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 7 (bases 1 to 166719)
AUTHORS Waterston,R.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 30, 2001 this sequence version replaced gi:13570009.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: saplens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0803A13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateo, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of RP11-803A13; actual end is at base position 166719 of RP11-803A13.

Sequence derived from PCR from base position 103627 to 103689.

FEATURES

Source

1.166719
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-803A13"
 /clone_lib="RPc1-11"
 1074..11102
 /rpt_family="AT-rich"
 1480..2050
 /note="similar to EST A1806700 (NID:g5393266) wF35f06.x1"
 1634..2034
 /note="similar to EST D59310 (NID:g960416)"
 2010..2233
 /rpt_family="ERV1"
 2234..2745
 /rpt_family="ERV1"
 2766..2816
 /rpt_family="(CA)n"
 2869..3044
 /rpt_family="ERV1"
 3039..3063
 /rpt_family="(A)n"
 3253..4065
 /rpt_family="L1"
 4159..4236
 repeat_region

/rpt_family="(TA)n"
 4368..4530
 /rpt_family="MER1_type"
 repeat_region
 4555..4582
 /rpt_family="(TTTG)n"
 repeat_region
 4589..4836
 /rpt_family="Alu"
 repeat_region
 5809..6027
 /rpt_family="MIR"
 repeat_region
 6195..6277
 /rpt_family="MER1_type"
 repeat_region
 6281..6328
 /rpt_family="L1"
 repeat_region
 6329..6647
 /rpt_family="Alu"
 repeat_region
 6620..6647
 /rpt_family="(A)n"
 repeat_region
 6648..6728
 /rpt_family="L1"
 repeat_region
 6779..7265
 /note="similar to EST AA576508 (NID:g2354008) nm76c09.s1"
 6787..6975
 /rpt_family="L2"
 repeat_region
 7307..7356
 /rpt_family="(T)n"
 repeat_region
 7327..7634
 /rpt_family="Alu"
 repeat_region
 7696..8005
 /rpt_family="Alu"
 repeat_region
 7864..7886
 /rpt_family="(T)n"
 repeat_region
 7889..8332
 /note="similar to EST A1625794 (NID:g4650737) ty67d04.x1"
 8277..8751
 /note="similar to EST BF059443 (NID:g10813261)"
 9133..9291
 /rpt_family="MIR"
 repeat_region
 9275..9461
 /note="similar to EST AA704040 (NID:g2713958) ag81f10.r1"
 9616..10006
 /rpt_family="MALR"
 repeat_region
 10039..10130
 /rpt_family="MALR"
 repeat_region
 10299..10638
 /note="similar to EST AA005136 (NID:g1448639) zh95e03.s1"
 10491..10638
 /note="similar to EST A1078188 (NID:g3412596) cz12f08.x1"
 10649..11134
 /rpt_family="ERVK"
 repeat_region
 11136..11408
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 11136..11408
 /note="similar to EST A1078188 (NID:g3412596) cz12f08.x1"
 11333..11414
 /rpt_family="L2"
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 12686..12928
 /rpt_family="L1"
 repeat_region
 12716..13320
 /note="similar to EST AM972049 (NID:g8161790)"
 13324..13671
 /note="similar to EST BG181175 (NID:g13702947)"
 13326..13674
 /note="similar to EST AA905638 (NID:g3040961) oj87c08.s1"
 13842..14185
 /note="similar to EST AA904412 (NID:g3039353) ok07e01.s1"
 14316..14795
 /note="similar to EST AM293618 (NID:g6700254)"
 14518..14703
 /note="similar to EST A1352084 (NID:g4089290) qr10b01.x1"
 14668..15090
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 15359..15906
 /rpt_family="L1"
 repeat_region

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XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
XX
XX WPI: 1996-412774/41.
DR P-PSDB; AAM00738.
XX
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
XX
XX Example 3: Page 47-48; 113pp; English.
XX
CC 3 CDNA clones (AA13611-13) code for splice variants (AAM00726-28)
CC of the human vascular endothelial growth factor-like polypeptide
CC SOM175 (see also AAM00725). They were identified in a human foetal
CC spleen library and respectively lack exon 6, exons 6+7, and exon 4
CC of the SOM175 gene (see also AA13610). The CDNA clones can be
CC used to produce recombinant SOM175 proteins that are useful for
CC inducing astroglial proliferation and for promoting neural survival
CC and/or proliferation.
CC
XX
SQ Sequence 910 BP; 182 A; 316 C; 254 G; 158 T; 0 other;

Query Match 91.3%; Score 27.4; DB 17; Length 910;
Best Local Similarity 96.6%; Pred. No. 0.03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctggcagcagcagtcgcgagtcgagtc 29
|||||
Db 277 ctggcagcagcagtcgcgagtcgagtc 305

RESULT 2
AA15763
ID AA15763 standard; DNA; 531 BP.
XX
AC AA15763;
XX
XX 19-JUN-2000 (first entry)
XX
DE DNA encoding VEGF-3 homologue, SEQ ID NO:21.
XX
KW Vascular endothelial growth factor 3; VEGF-3; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.
XX
OS Homo sapiens.
XX
PN WO200009148-A1.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-US18054.
XX
PR 10-AUG-1998; 98US-0132088.
PR 10-FEB-1999; 99US-0244694.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Hu J, Olsen HS, Rosen CA;
XX
XX WPI: 2000-224173/19.
XX
XX

PT New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -
XX
XX Disclosure; Page 137; 209pp; English.

CC The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AA194802), a splice variant of human VEGF-3 (AA194806), and
CC nucleic acids encoding them (AA15748, AA15762). The CDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line CDNA library.
CC The CDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AA15761-AA15880 represent DNA
CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.
XX
SQ Sequence 531 BP; 111 A; 162 C; 163 G; 95 T; 0 other;

Query Match 90.0%; Score 27; DB 21; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcagcagcagtcgcgagtcgagtc 30
|||||
Db 191 ggcagcagcagtcgcgagtcgagtc 217

RESULT 3
AA137912
ID AA137912 standard; CDNA; 405 BP.
XX
AC AA137912;
XX
XX 28-APR-1997 (first entry)
XX
DE VEGF-B112 coding sequence.
XX
KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse; ss.
XX
XX Mus musculus.
XX
PN WO9626736-A1.
XX
PD 06-SEP-1996.
XX
PF 01-MAR-1996; 96WO-US02957.
XX
PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alitalo K, Eriksson U, Olofsson B, Pajusola K;
XX
XX WPI: 1996-412582/41.
XX
XX P-PSDB; AAM04828.
XX
XX

PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX Claim 1; Page 57; 107pp; English.

CC AAT37909-T37915 represent the coding sequences for the vascular
 CC endothelial growth factor (VEGF) proteins of the invention, which promote
 CC glycosylated cationic dimer, and is sometimes referred to as vascular
 CC permeability factor (VPF). VEGF has diverse effects, depending on the
 CC specific biological context in which it is found. VEGF is a potent
 CC angiogenesis in vivo by promoting endothelial cell growth during normal
 CC embryonic development, wound healing, and tissue
 CC regeneration/reorganisation. The VEGF proteins of the invention share
 CC the angiogenic and other properties of VEGF, but are distributed and
 CC expressed in tissues differently to VEGF. The proteins can therefore be
 CC used to accelerate angiogenesis in wound healing. Antibodies against the
 CC proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.

XX Sequence 405 BP; 93 A; 113 C; 120 G; 79 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctgggcagcaccacgaatccgaatcgatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 278 ctgggcagcaccacgaatccgaatcgatcc 307

RESULT 4
 AAV63566
 ID AAV63566 standard; cDNA; 405 BP.
 XX
 AC AAV63566;
 XX
 DT 29-JAN-1999 (first entry)
 XX
 DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B112.
 XX
 KM Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KM endothelial cell; angiogenesis; tissue growth; organ repair; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 4..405
 FT /tag= a
 FT /product= VEGF-B112
 XX
 PN US5840693-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 01-MAR-1996; 9605-0609443.
 XX
 PR 01-MAR-1996; 9605-0609443.
 PR 01-MAR-1995; 9505-0397651.
 PR 06-JUN-1995; 9505-0469427.
 PR 06-DEC-1995; 9505-0569063.
 XX
 PA (LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
 XX
 DR WPI; 1999-034079/03.
 DR P-PDB; AAW04826.
 XX

PT Vascular endothelial growth factor-B isoforms, and DNA encoding
 PT them - useful for inducing angiogenesis and cellular proliferation,
 PT and raising antibodies to inhibit activities in e.g. tumours
 XX
 PS Claim 22; Fig 7; 52pp; English.

XX
 CC The present sequence encodes murine vascular endothelial growth factor
 CC (VEGF)-B112. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries form pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.

XX Sequence 405 BP; 93 A; 113 C; 120 G; 79 T; 0 other;

Query Match 89.3%; Score 26.8; DB 20; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctgggcagcaccacgaatccgaatcgatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 278 ctgggcagcaccacgaatccgaatcgatcc 307

RESULT 5
 AAT37910
 ID AAT37910 standard; cDNA; 565 BP.
 XX
 AC AAT37910;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE Adult heart VEGF-B167 coding sequence.
 XX
 KM Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KM VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KM vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KM embryonic development; wound healing; tissue reorganisation; antibody;
 KM cancer; metastatic risk; tumour cell; mouse; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS WO9626736-A1.
 FT /tag= a
 FT /product= VEGF-B167
 XX
 PN WO9626736-A1.
 XX
 PD 06-SEP-1996.
 XX
 PF 01-MAR-1996; 96WO-0502957.
 XX
 PR 06-DEC-1995; 9505-0569063.
 PR 01-MAR-1995; 9505-0397651.
 PR 06-JUN-1995; 9505-0469427.
 XX
 PA (LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
 XX
 DR WPI; 1996-412562/41.
 DR P-PDB; AAW04826.
 XX
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 XX
 PS Claim 1; Page 54-55; 107pp; English.
 XX
 CC AAT37909-T37915 represent the coding sequences for the vascular

CC endothelial growth factor (VEGF) proteins of the invention, which promote
CC endothelial or mesodermal cell proliferation. VEGF is also a
CC glycosylated cationic dimer, and is sometimes referred to as vascular
CC permeability factor (VPF). VEGF has diverse effects, depending on the
CC specific biological context in which it is found. VEGF is a potent
CC angiogenesis in vivo by promoting endothelial cell growth during normal
CC embryonic development, wound healing, and tissue
CC regeneration/reorganisation. The VEGF proteins of the invention share
CC the angiogenic and other properties of VEGF, but are distributed and
CC expressed in tissues differently to VEGF. The proteins can therefore be
CC used to accelerate angiogenesis in wound healing. Antibodies against the
CC proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences direct against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.

SQ Sequence 565 BP; 120 A; 179 C; 166 G; 100 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.05;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccacgaatccgagtcagatcc 30
||||||| ||||||| ||||||| ||||||| |||
DB 273 ctgggcagcaccacgaatccgagtcagatcc 302

RESULT 5
ID AAV63564 standard; cDNA; 565 BP.
XX AAV63564;
AC
XX
DT 29-JAN-1999 (first entry)
DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B167.
XX
XX Vascular endothelial growth factor; VEGF; proliferation; mouse;
KM endothelial cell; angiogenesis; tissue growth; organ repair; ss.
KW
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 1..565
FT CDS /*tag= a
FT /product= VEGF-B167
FT /transl_except= (pos:1, aa: Met)

XX US5840693-A.
XX PD 24-NOV-1998.

XX PF 01-MAR-1996; 96US-0609443.
XX PR 01-MAR-1996; 96US-0609443.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
PR 06-DEC-1995; 95US-0569063.

XX PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX WPI: 1999-034079/03.
DR P-PSDB; AAM80490.
XX

PT Vascular endothelial growth factor-B isoforms, and DNA encoding
PT them - useful for inducing angiogenesis and cellular proliferation,
PT and raising antibodies to inhibit activities in e.g. tumours

PS Claim 22; Fig 3; 52pp; English.

XX
XX The present sequence encodes murine vascular endothelial growth factor
CC (VEGF)-B167. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
CC new blood supplies to grow and proliferate.

SQ Sequence 565 BP; 120 A; 179 C; 166 G; 100 T; 0 other;

Query Match 89.3%; Score 26.8; DB 20; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.05;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccacgaatccgagtcagatcc 30
||||||| ||||||| ||||||| ||||||| |||
DB 273 ctgggcagcaccacgaatccgagtcagatcc 302

RESULT 7
ID AAT37914 standard; cDNA; 624 BP.
XX AAT37914;
AC
XX
DT 28-APR-1997 (first entry)
XX
DE VEGF-B186 coding sequence.

XX
XX Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KM VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KM vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse; ss.
XX
XX

OS Mus musculus.

XX
XX W09626736-A1.

XX PD 06-SEP-1996.

XX PF 01-MAR-1996; 96WO-US02957.
XX PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.

XX PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX WPI: 1996-412582/41.
DR P-PSDB; AAM04830.

XX Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis

XX Claim 1; Page 60; 107pp; English.

XX AAT37909-r37915 represent the coding sequences for the vascular

CC endothelial growth factor (VEGF) proteins of the invention, which promote
CC endothelial or mesodermal cell proliferation. VEGF is also a
CC glycosylated cationic dimer, and is sometimes referred to as vascular
CC permeability factor (VPF). VEGF has diverse effects, depending on the
CC specific biological context in which it is found. VEGF is a potent
CC endothelial cell mitogen, and directly contributes to induction of
CC angiogenesis in vivo by promoting endothelial cell growth during normal
CC embryonic development, wound healing, and tissue
CC regeneration/reorganisation. The VEGF proteins of the invention share
CC the angiogenic and other properties of VEGF, but are distributed and
CC expressed in tissues differently to VEGF. The proteins can therefore be
CC used to accelerate angiogenesis in wound healing. Antibodies against the
CC proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences directed against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.

SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;
Query Match 89.3%; Score 26.8; DB 17; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ctgggcagcaccacgaatccgatcgatccagatcc 30
||||| ||||||| ||||||| |||||||
DB 275 ctgggcacaccacgaatccgatcgatccagatcc 304

RESULT 8
AAV63568
ID AAV63568 standard; cDNA; 624 BP.
XX
AC AAV63568;
XX
DT 29-JAN-1999 (first entry)
XX
DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B186.
XX
KM Vascular endothelial growth factor; VEGF: proliferation; mouse;
KM endothelial cell; angiogenesis; tissue growth; organ repair; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..624
FT /*tag= a
FT /product= VEGF-B186
XX
PN US5840693-A.
XX
PD 24-NOV-1998.
XX
PF 01-MAR-1996; 96US-0609443.
XX
PR 01-MAR-1996; 96US-0609443.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0468427.
PR 06-DEC-1995; 95US-0569063.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Altalo K, Eriksson U, Olofsson B, Pajusola K;
XX WPI; 1999-034079/03.
DR P-PSDB; AAB80494.
XX
PT Vascular endothelial growth factor-B isoforms, and DNA encoding

PT them - useful for inducing angiogenesis and cellular proliferation,
PT and raising antibodies to inhibit activities in e.g. tumours
XX
PS Claim 22; Fig 12; 52pp; English.
XX

CC The present sequence encodes murine vascular endothelial growth factor
CC (VEGF)-B186. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
CC new blood supplies to grow and proliferate.

SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;
Query Match 89.3%; Score 26.8; DB 20; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatccgatcgatccagatcc 30
||||| ||||||| ||||||| |||||||
DB 275 ctgggcacaccacgaatccgatcgatccagatcc 304

RESULT 9
AAC81776
ID AAC81776 standard; DNA; 624 BP.
XX
AC AAC81776;
XX
DT 23-FEB-2001 (first entry)
XX

DE Human vascular endothelial growth factor VEGF-B186 coding sequence.

XX Human; vascular endothelial growth factor; VEGF-B; bone growth;
KM angiogenesis; neovascularisation; bone break; inflammation; ds.
XX

OS Homo sapiens.

PN WO200064261-A1.

XX 02-NOV-2000.

PD 26-APR-2000; 2000MO-US11096.

PF 26-APR-1999; 99US-0130935.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Aase K, Kaipainen A, Olofsson B, Altalo K, Eriksson U;

XX WPI; 2001-015797/02.

DR P-PSDB; AAB36296.

PT Use of a polypeptide having the biological activity of vascular
PT endothelial growth factor-B for stimulating angiogenesis of bone,
PT healing of bone fractures and enhancing acceptance of an implant to
PT bone _
XX

PS Disclosure: Page 36-37; 43pp; English.

CC The present invention discloses a use for human vascular endothelial
CC growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This
CC can be used to promote bone growth, stimulate the healing of breaks or
CC fractures, secure an implant to the bone and to alleviate inflammation in
CC long bones.
XX

SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

Query Match Best Local Similarity 89.3%; Score 26.8; DB 22; Length 624;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 ctgggcacaccagtcgcgatgcagatcc 304

RESULT 10

AAC81777 ID AAC81777 standard; cDNA; 624 BP.

XX AAC81777;

XX 23-FEB-2001 (first entry)

XX Murine vascular endothelial growth factor VEGF-B186 coding sequence.

XX Mouse; vascular endothelial growth factor; VEGF-B; bone growth;

XX angiogenesis; neovascularisation; bone break; inflammation; ss.

XX Mus sp.

XX WO200064261-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-US1096.

XX 26-APR-1999; 99US-0130935.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Aase K, Kaipainen A, Olofsson B, Alltalo K, Eriksson U;

XX WPI: 2001-015797/02.

XX Use of a polypeptide having the biological activity of vascular

XX endothelial growth factor-B for stimulating angiogenesis of bone,

XX healing of bone fractures and enhancing acceptance of an implant to

XX bone -

XX Disclosure; Page 38-39; 43pp; English.

XX The present invention discloses a use for human vascular endothelial

XX growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This

XX can be used to promote bone growth, stimulate the healing of breaks or

XX fractures, secure an implant to the bone and to alleviate inflammation in

XX long bones.

XX Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

XX Query Match Best Local Similarity 89.3%; Score 26.8; DB 22; Length 624;

XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 ctgggcacaccagtcgcgatgcagatcc 304

RESULT 11

AAT37909 ID AAT37909 standard; cDNA; 886 BP.

XX AAT37909;

XX

DT 28-APR-1997 (first entry)

XX Partial VEGF-B coding sequence.

XX Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;

XX VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;

XX vascular permeability factor; cell mitogen; angiogenesis; cell growth;

XX embryonic development; wound healing; tissue reorganisation; antibody;

XX cancer; metastatic risk; tumour cell; mouse; ss.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 2..312

XX CDS /*tag= a

XX CDS /product= First reading frame VEGF-B fragment

XX CDS 312..479

XX CDS /*tag= b

XX CDS /product= Second reading frame VEGF-B fragment

XX WO9626736-A1.

XX 06-SEP-1996.

XX 01-MAR-1996; 96WO-US02957.

XX 06-DEC-1995; 95US-0569063.

XX 01-MAR-1995; 95US-0397651.

XX 06-JUN-1995; 95US-0469427.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Alltalo K, Eriksson U, Olofsson B, Rajusola K;

XX WPI: 1996-412582/41.

XX P-PSDB: AAW04824, AAW04825.

XX Vascular endothelial growth factor VEGF-B proteins - useful to

XX accelerate angiogenesis in wound healing, also related nucleic acid

XX and antibodies for cancer diagnosis

XX Claim 1; Page 53; 107pp; English.

XX This represents a fragment of the mouse embryo vascular endothelial

XX growth factor-B (VEGF-B) protein coding sequence. The encoded proteins

XX (and AAW04825-WO4831) represent the VEGF proteins of the invention, and

XX promote endothelial or mesodermal cell proliferation. VEGF is also a

XX glycosylated cationic dimer, and is sometimes referred to as vascular

XX permeability factor (VPF). VEGF has diverse effects, depending on the

XX specific biological context in which it is found. VEGF is a potent

XX endothelial cell mitogen, and directly contributes to induction of

XX angiogenesis in vivo by promoting endothelial cell growth during normal

XX embryonic development, wound healing, and tissue

XX regeneration/reorganisation. The VEGF proteins of the invention share

XX the antigenic and other properties of VEGF, but are distributed and

XX expressed in tissues differently to VEGF. The proteins can therefore be

XX used to accelerate angiogenesis in wound healing. Antibodies against

XX the proteins can be used for inhibiting angiogenesis. The antibodies

XX can also be used diagnostically to quantitatively detect VEGF-B.

XX Primers complementary to the coding sequences for the proteins of the

XX invention can also be used to detect VEGF-B coding sequences.

XX Identification of VEGF-B in cancer biopsy specimens may be useful as an

XX indicator of metastatic risk. VEGF-B expression in a cell can be

XX retarded using antisense sequences directed against the VEGF coding

XX sequences, this is especially useful in retarding VEGF expression in

XX tumour cells.

XX Sequence 886 BP; 227 A; 261 C; 226 G; 172 T; 0 other;

XX Query Match Best Local Similarity 89.3%; Score 26.8; DB 17; Length 886;

XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

Sequence 886 BP: 227 A: 261 C: 226 G: 172 T: 0 other:

CC adult mice. VRF169 lacks exon 6, found in VRF186 cDNA (AAT13809).

Sequence 1141 BP; 256 A; 361 C; 313 G; 211 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 1141;
 Best Local Similarity 93.3%; Pred. No. 0.056;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatccgagtcagatcc 30
 ||||||| ||||||| ||||||| |||||||
 Db 440 ctgggcacacccaagtcgagtcagatcc 469

RESULT 14

AA13809
 ID AA13809 standard; cDNA, 1242 BP.

AC AAT13809;
 DT 30-NOV-1996 (first entry)
 XX

DE Murine VRF186 cDNA.

XX VRF; vascular endothelial growth factor; VEGF; SOM175; neuron;
 KM astroglial proliferation; ss.
 XX

OS Mus musculus.

XX Key Location/Qualifiers
 FH CDS 166..789
 FT /*tag= a

FT sig_peptide 166..228
 FT /*tag= b

FT mat_peptide 229..786
 FT /*tag= c

FT exon 576..676
 FT /*tag= d

FT repeat_region 1163..1176
 FT /*note= "exon 6, deleted in VRF169"

FT /*tag= e

FT /*note= "polymorphic AC repeat region"
 FT 1186..1191

FT /*tag= f

XX MO9627007-A1.

XX 06-SEP-1996.

XX 22-FEB-1996; 96WO-AU00094.

XX 22-DEC-1995; 95AU-0007274.

XX 02-MAR-1995; 95AU-0001457.

XX 20-NOV-1995; 95AU-0006647.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;

XX WPI: 1996-412774/41.

XX P-PSDB; AAM00863.

XX New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival

XX Example 5; Fig 9; 113pp; English.

XX VRF186 cDNA (AA13809) codes for the murine homologue (AAM00863) of
 CC human vascular endothelial growth factor-like polypeptide SOM175
 CC (AAM00725), a protein capable of inducing astroglial proliferation
 CC and of promoting neural survival and/or proliferation. It was
 CC obt'd. from a new-born mouse brain cDNA library using SOM175 cDNA
 CC (see also AA133610) as probe. The murine VRF gene maps near to the
 CC centromere of chromosome 19. It is highly expressed in embryo tissue
 CC and in the heart and brown fat of adult mice. An alternatively

CC spliced variant, VRF169 (AA13810), was also identified.
 XX
 SQ Sequence 1242 BP; 272 A; 409 C; 333 G; 228 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 1242;
 Best Local Similarity 93.3%; Pred. No. 0.057;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatccgagtcagatcc 30
 ||||||| ||||||| ||||||| |||||||
 Db 440 ctgggcacacccaagtcgagtcagatcc 469

RESULT 15

AA15764
 ID AA15764 standard; DNA; 445 BP.

AC AA15764;
 DT 19-JUN-2000 (first entry)
 XX

DE DNA encoding VEGF-3 homologue, SEQ ID NO:22.

XX

XX Vascular endothelial growth factor 3; VEGF-3; homologue;
 KM vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
 KM cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.
 XX

OS Homo sapiens.

XX WO200009148-A1.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18054.

XX 10-AUG-1998; 98US-0132088.

XX 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hu J, Olsen HS, Rosen CA;

XX WPI: 2000-224173/19.

XX New human gene encoding vascular endothelial growth factor 3 and
 PT polypeptide encoded by the gene is useful for treating various
 PT disorders associated with vascular and lymphatic system -

XX Disclosure; Page 137-138; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3
 CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806) and
 CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding
 CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
 CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
 CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
 CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
 CC being consistent with vascular and lymphatic specific expression. VEGF-3
 CC proteins and nucleotides are useful in preventing, treating or the
 CC ameliorating various disorders and conditions associated with the
 CC vascular and lymphatic systems. These conditions and disorders include
 CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
 CC disease. VEGF-3 may also be used to identify its own binding partners.
 CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
 CC an alternative to restriction fragment length polymorphism (RFLP). The
 CC nucleotides are also useful to prepare PCR primers for amplifying an
 CC isolating selected DNAs. Sequences AA15763-A15880 represent DNA
 CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.
 XX Sequence 445 BP; 86 A; 170 C; 120 G; 69 T; 0 other;

Query Match 86.7%; Score 26; DB 21; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gcagcaccagtcgcgatgcagatcc 30
 ||||||||||||||||||
 DB 79 gcagcaccagtcgcgatgcagatcc 104

RESULT 16

AAT37911
 ID AAT37911 standard; cDNA; 591 BP.

AC AAT37911;

DT 28-APR-1997 (first entry)

DE Adult heart VEGF-B174 coding sequence.

XX Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
 KM VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KM vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KM embryonic development; wound healing; tissue reorganisation; antibody;
 KM cancer; metastatic risk; tumour cell; mouse; ss.

XX Mus musculus.

PN WO9626736-A1.

PD 06-SEP-1996.

PF 01-MAR-1996; 96WO-US02957.

XX 06-DEC-1995; 95US-0569063.

PR 01-MAR-1995; 95US-0397651.

PR 06-JUN-1995; 95US-0469427.

XX (LUDWIG) INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

PI Altalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI: 1996-412582/41.

XX P-PSDB: AAM04827.

PS Claim 1; Page 56; 107pp; English.

CC AAT37909-T37915 represent the coding sequences for the vascular
 CC endothelial growth factor (VEGF) proteins of the invention, which promote
 CC endothelial or mesodermal cell proliferation. VEGF is also a
 CC glycosylated cationic dimer, and is sometimes referred to as vascular
 CC permeability factor (VPF). VEGF has diverse effects, depending on the
 CC specific biological context in which it is found. VEGF is a potent
 CC angiogenesis in vivo by promoting endothelial cell growth during normal
 CC embryonic development, wound healing, and tissue
 CC regeneration/reorganisation. The VEGF proteins of the invention share
 CC the angiogenic and other properties of VEGF, but are distributed and
 CC expressed in tissues differently to VEGF. The proteins can therefore be
 CC used to accelerate angiogenesis in wound healing. Antibodies against the
 CC proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.

SO Sequence 591 BP; 126 A; 186 C; 174 G; 105 T; 0 other;

Query Match 78.7%; Score 23.6; DB 17; Length 591;
 Best Local Similarity 86.7%; Pred. No. 1.2;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctggcagcaccagtcgcgatgcagatcc 30
 ||||||| ||||||| ||||||| |||||||
 DB 278 ctggcagcaccagtcgcgatgcagatcc 307

RESULT 17

AAV63565
 ID AAV63565 standard; cDNA; 591 BP.

AC AAV63565;

DT 29-JAN-1999 (first entry)

DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B174.

XX Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KM endothelial cell; angiogenesis; tissue growth; organ repair; ss.

XX Mus sp.

OS Key Location/Qualifiers

FN CDS 4..591

FT /*tag- a

FT /product= VEGF-B174

PN US5840693-A.

PD 24-NOV-1998.

PF 01-MAR-1996; 96US-0609443.

XX 01-MAR-1996; 96US-0609443.

PR 01-MAR-1995; 95US-0397651.

PR 06-JUN-1995; 95US-0469427.

XX 06-DEC-1995; 95US-0569063.

PA (LUDWIG) INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

PI Altalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI: 1999-034079/03.

XX P-PSDB: AAM80491.

PS Claim 22; Fig 5; 52pp; English.

CC The present sequence encodes murine vascular endothelial growth factor
 CC (VEGF)-B174. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries form pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.

CC Sequence 591 BP; 126 A; 186 C; 174 G; 105 T; 0 other;

Query Match 78.7%; Score 23.6; DB 20; Length 591;

Best Local Similarity 86.7%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctgggcagcaccgaatccgagtcagatcc 30
||||| ||||||| ||||||| |||
Db 278 ctgggcagcaccgaatccgagtcagatcc 307

RESULT 18
AAAI5766
ID AAAI5766 standard; DNA: 423 BP.

XX
AC AAAI5766;

XX 19-JUN-2000 (first entry)

XX DNA encoding VEGF-3 homologue, SEQ ID NO:24.

XX Vascular endothelial growth factor 3; VEGF-3; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.

XX Mus musculus.

XX WO200009148-A1.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18054.

XX 10-AUG-1998; 98US-0132088.

XX 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hu J, Olsen HS, Rosen CA;

XX WPI; 2000-224173/19.

XX New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -

XX Disclosure; Page 139-140; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AAAI5748, AAAI5762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AAAI5748 in
CC that the A at position 498 in AAAI5748 is not present in AAAI5762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AAAI5763-AI5880 represent DNA
CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.
XX
XX Sequence 423 BP; 96 A; 135 C; 123 G; 69 T; 0 other;

Query Match 74.0%; Score 22.2; DB 21; Length 423;
Best Local Similarity 88.9%; Pred. No. 4.4;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatccgagtcagatcc 30
||| ||||||| ||||||| |||

Db 52 ggcagcaccgaatccgagtcagatcc 78

RESULT 19

XX AAAI5881
ID AAAI5881 standard; DNA: 389 BP.

XX AAAI5881;

XX 19-JUN-2000 (first entry)

XX DNA encoding a homologue of VEGF-3 splice variant, SEQ ID NO:139.

XX Vascular endothelial growth factor 3; VEGF-3; splice variant; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.

XX Mus musculus.

XX WO200009148-A1.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18054.

XX 10-AUG-1998; 98US-0132088.

XX 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hu J, Olsen HS, Rosen CA;

XX WPI; 2000-224173/19.

XX New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -

XX Disclosure; Page 191; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AAAI5748, AAAI5762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AAAI5748 in
CC that the A at position 498 in AAAI5748 is not present in AAAI5762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AAAI5881-AI5895 represent DNA
CC sequences encoding homologues of the human VEGF-3 splice variant from
XX human, mouse and rat.

XX Sequence 389 BP; 89 A; 105 C; 117 G; 78 T; 0 other;

Query Match 69.3%; Score 20.8; DB 21; Length 389;
Best Local Similarity 91.7%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 agcaccgaatccgagtcagatcc 30
| ||||||| ||||||| |||
Db 270 aacaccgaatccgagtcagatcc 293

RESULT 20

AAK66306
ID AAK66306 standard; DNA; 2002 BP.
AC AAK66306;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21118.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUL-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0226886.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234474.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-483426/52.
DR
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 21118; 3071bp + Sequence Listing: English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2002 BP; 431 A; 506 C; 675 G; 390 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 2002;
Best Local Similarity 85.2%; Pred. No. 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ggcagcaccgaagtcgagtcgagatcc 30
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Db 1653 ggcagcaccatgctctcatgtgagatcc 1679

RESULT 21
AAK6307
ID AAK6307 standard; DNA; 2205 BP.
XX
AC AAK6307;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21119.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0232081.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241808.
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PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and

PT metastasis -
XX
PS Disclosure; SEQ ID NO 21119; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
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CC that affect the activity of (I) by expressing inactive proteins or to
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CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2205 BP; 466 A; 582 C; 732 G; 425 T; 0 other;
XX
Query Match 68.7%; Score 20.6; DB 22; Length 2205;
Best Local Similarity 85.2%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 ggcagcaccaatcgcgagtcgaatcc 30
Db 1856 ggcagcaccaatgctcctcatgagatcc 1882
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RESULT 22
AAK6308
ID AAK6308 standard; DNA; 22680 BP.
XX
AC AAK6308;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21120.
XX
KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; OS.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
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PR 08-SEP-2000; 2000US-0232081.
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PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
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PR 21-SEP-2000; 2000US-0234223.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.

PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX PA
XX Rosen CA, Bairash SC, Ruben SM;
PI WPI: 2001-483426/52.
XX
DR
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 21120; 3071bp + sequence listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
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CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. NO. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatccgcatgcagatcc 30
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Db 16682 ggcagcaccatgtctcatgcagatcc 16708

RESULT 23

AAK73334
ID AAK73334 standard; DNA; 22680 BP.

XX AAK73334;

XX 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28146.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

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PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

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PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214866.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

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PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

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PR 14-AUG-2000; 2000US-0225266.

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PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 23-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227099.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231244.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
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PR 08-SEP-2000; 2000US-0232081.
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PR 05-JAN-2001: 2000US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI, 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX PS Disclosure; SEQ ID NO 28156; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
OS
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XX WO200157182-A2.
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XX 31-JAN-2000; 2000US-0179065.
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PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
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XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 28437; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
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CC treatment of diseases associated with inappropriate (I) expression. For
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CC protein. (I) proteins and polynucleotides may be used to prevent, CC
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human Immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4555 A; 7046 C; 6635 G; 4444 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
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XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;

KM cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

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XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33162.
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XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
XX WO200157182-A2.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.

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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249218.
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PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
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PR 01-DEC-2000; 2000US-0250391.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.

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PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 33162; 3071pp + Sequence listing; English.
XX
XX AAK51951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccaagtcgcgagtcagatcc 30
Db 16682 ggcagcacatgtcctcatgtgagatcc 16708

RESULT 29
ABA70982
ID ABA70982 standard; DNA; 197 BP.
XX
AC ABA70982;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #19287.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
```

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PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human foetal liver -
XX
PS Claim 4; SEQ ID NO 19287; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccaagtcgcgagtcagatcc 29
Db 62 ggcagcaccaagcccggtgagctc 87

RESULT 30
ABA37402
ID ABA37402 standard; DNA; 197 BP.
XX
AC ABA37402;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #15868 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
```

XX Claim 4; SEQ ID No 15868; 530pp; English.
XX
PS
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcggatgcagatc 29
|||||
DB 62 ggcagcaccgaagtcggatgcagatc 87

RESULT 31
AAK19258
ID AAK19258 standard; DNA; 197 BP.
XX
AC AAK19258;
XX
DE 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 19249.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN MO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 19249; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcggatgcagatc 29
|||||
DB 62 ggcagcaccgaagtcggatgcagatc 87

RESULT 32
AAK45228
ID AAK45228 standard; DNA; 197 BP.
XX
AC AAK45228;
XX
DE 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 19785.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN MO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 19785; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcggatgcagatc 29
|||||
DB 62 ggcagcaccgaagtcggatgcagatc 87

RESULT	33
ID	AAI25200 standard; DNA; 197 BP.
XX	
AC	AAI25200;
XX	
DT	12-OCT-2001 (first entry)
DE	Probe #15133 for gene expression analysis in human cervical cell sample.
XX	
KW	Probe; human; microarray; gene expression; cervical epithelial cell;
RW	cervical cancer; ss.
XX	
OS	Homo sapiens.
PN	WO200157278-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US00670.
XX	
PR	04-FEB-2000; 2000US-0180312.
PR	26-MAY-2000; 2000US-0207456.
PR	30-JUN-2000; 2000US-0608408.
PR	03-AUG-2000; 2000US-0633366.
PR	21-SEP-2000; 2000US-0234687.
PR	27-SEP-2000; 2000US-0236359.
PR	04-OCT-2000; 2000GB-0024263.
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-488901/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for
XX	analyzing gene expression in human cervical epithelial cells -
PS	Claim 25; SEQ ID No 15133; 487bp; English.
XX	
CC	The present invention relates to human single exon nucleic acid probes
CC	(SENP). The present sequence is one such probe. The SENPs are derived
CC	from human HeLa cells. The SENPs can be used to produce a single exon
CC	microarray, which can be used for measuring human gene expression in a
CC	sample derived from human cervical epithelial cells. By measuring gene
CC	expression, the probes are therefore useful in grading and/or staging
CC	of diseases of the cervix, notably cervical cancer.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
SQ	Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;
Query Match	65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity	84.6%; Pred. No. 50;
Matches 22; Conservative 0;	Indels 4; Gaps 0;
OY	4 ggcagcaccacgaatccgatgcagatc 29
Db	62 ggcagcaccacgaagcccgggtgagaacctc 87
RESULT	34
ID	AAI51179 standard; DNA; 197 BP.
XX	
AC	AAI51179;
XX	
DT	17-OCT-2001 (first entry)
XX	

DE	Probe #19865 used to measure gene expression in human placenta sample.
XX	
KW	Probe; microarray; human; placenta; antenatal diagnosis;
KW	genetic disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200157272-A2.
PD	
XX	
PF	09-AUG-2001.
XX	
XX	
PR	30-JAN-2001; 2001WO-US000663.
XX	
PR	04-FEB-2000; 2000US-0180312.
XX	
PR	26-MAY-2000; 2000US-0207456.
XX	
PR	30-JUN-2000; 2000US-0608408.
XX	
PR	03-AUG-2000; 2000US-0632366.
XX	
PR	21-SEP-2000; 2000US-0234687.
XX	
PR	27-SEP-2000; 2000US-0236359.
XX	
PR	04-OCT-2000; 2000GB-0024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI: 2001-488897/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for
PT	analyzing gene expression in human placenta -
XX	
PS	Claim 25; SEQ ID NO 19865; 654bp; English.
XX	
CC	The present invention relates to single exon nucleic acid probes (SENP).
CC	The present sequence is one such probe. The probes are useful for
CC	producing a microarray for predicting, measuring and displaying gene
CC	expression in samples derived from human placenta. The probes are useful
CC	for antenatal diagnosis of human genetic disorders.
XX	
SQ	Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;
Query Match	65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity	84.6%; Pred. No. 50;
Matches 22; Conservative	0; Mismatches 4; Indels 0; Gaps 0.
QY	4 ggcagaccacgaatccgagtcagatc 29
Db	62 ggcagaccacgaatccgagtcagatc 87
RESULT 35	
ABA58386	
ID	ABA58386 standard; DNA; 486 BP.
XX	
AC	ABA58386;
XX	
DT	01-FEB-2002 (first entry)
XX	
DE	Human foetal liver single exon nucleic acid probe #6691.
XX	
KW	Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200157277-A2.
XX	
PD	
XX	
PF	09-AUG-2001.
XX	
XX	
PR	30-JAN-2001; 2001WO-US00069.
XX	
PR	04-FEB-2000; 2000US-0180312.
XX	
PR	26-MAY-2000; 2000US-0207456.
XX	
PR	30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
PS Claim 1; SEQ ID NO 6691; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaagtcggatgcagatc 29
|||||
DB 324 ggcagaccacgaagtcggatgcagatc 349

RESULT 36

ABA27497
ID ABA27497 standard; DNA; 486 BP.

XX
AC ABA27497;

XX
DT 23-JAN-2002 (first entry)

DE Probe #5963 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.
XX

OS Homo sapiens.
XX

XX WO200157274-A2.
PN

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US00666.

XX
PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
PA

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

XX
DR WPI; 2001-488899/53.

XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 5963; 530pp; English.
PS
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaagtcggatgcagatc 29
|||||
DB 324 ggcagaccacgaagtcggatgcagatc 349

RESULT 37

AAK06491
ID AAK06491 standard; DNA; 486 BP.

XX
AC AAK06491;

XX
DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 6482.

XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer; ss.
XX

OS Homo sapiens.
XX

XX WO200157275-A2.
PN

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US00667.

XX
PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
PA

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

XX
DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX

XX Example 4; SEQ ID NO: 6482; 650pp + Sequence listing; English.
PS

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match

65.3%; Score 19.6; DB 22; Length 486;

Best Local Similarity 84.6%; Pred. No. 58;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ggcagaccacgaagtcgcgatgcagatc 29

Db 324 ggcagaccacgaagcccggtgagatc 349

RESULT 38

AAK32172

ID AAK32172 standard; DNA; 486 BP.

XX AAK32172;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 6729.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

OS Homo sapiens.

FN WO200157276-A2.

PD 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI: 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

PS Example 4; SEQ ID NO: 6729; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

QY 4 ggcagaccacgaagtcgcgatgcagatc 29

Db 324 ggcagaccacgaagcccggtgagatc 349

RESULT 39

AAI15983

ID AAI15983 standard; DNA; 486 BP.

XX AAI15983;

DT 12-OCT-2001 (first entry)

DE Probe #5916 for gene expression analysis in human cervical cell sample.

KW Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

OS Homo sapiens.

FN WO200157278-A2.

PD 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI: 2001-488901/53.

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human cervical epithelial cells -

PS Claim 25; SEQ ID NO 5916; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match

65.3%; Score 19.6; DB 22; Length 486;

Best Local Similarity 84.6%; Pred. No. 58;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ggcagaccacgaagtcgcgatgcagatc 29

Db 324 ggcagaccacgaagcccggtgagatc 349

RESULT 40

AAI38021

ID AAI38021 standard; DNA; 486 BP.

XX AAI38021;

```
XX 17-OCT-2001 (first entry)
XX
XX Probe #6707 used to measure gene expression in human placenta sample.
DE
XX Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 6707; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;
SQ
Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ggcagcaccacgctcggatgcagatc 29
DB 324 ggcagcaccacgctcggatgcagatc 349
RESULT 41
AAV02997/c
ID AAV02997 standard; cDNA; 1956 BP.
XX
XX AAV02997;
XX
XX 06-JUL-1998 (first entry)
XX
XX Murine Ena-VASP like (Evl) cDNA.
XX
XX Ena-VASP like; Evl gene; Mena; mammalian Ena; Enabled;
KW cytoskeleton; cell morphology; cell adhesion; cell motility;
KW cell growth; cell differentiation; ds.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 418..1599
XX FT /*tag= a
XX
```

```
PN WO9801755-A1.
XX
XX 15-JAN-1998.
XX
XX 03-JUL-1997; 97WO-US11669.
XX
XX 05-JUL-1996; 96US-0675815.
XX
XX (GBF) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX (HUTC-) HUTCHINSON CANCER RES CENT FRID.
XX
XX Gertler FB, Niebuhr K, Soriano P, Wehland J;
XX
XX WPI; 1998-101197/09.
XX P-PSDB; AAW37149.
XX
XX Detection of modulators of Mena and Ena-VASP-like genes and proteins
XX - used in control of cytoskeletal dynamic events in normal and
XX abnormal cell morphology, adhesion, motility, growth and
XX differentiation
XX
XX Example 1; Page 66-67; 77pp; English.
XX
XX This cDNA comprises murine Ena-VASP like (Evl) cDNA that codes
XX for a 393-amino acid Evl protein (see W37149). It was isolated
XX from a mouse embryonic stem cell cDNA library using human EST
XX clone T80305 as probe; the EST had been identified using a novel
XX mammalian Ena (Mena, see V02996) sequence to search the GenBank
XX database. 2 Novel mammalian genes, Mena and Evl, encoding Mena
XX (see W37148) and Evl are disclosed. Mena and Evl proteins have a
XX discrete, EVH1 functional domain responsible for Mena binding to
XX Listeria, and to the cytoskeletal proteins zyxin and vinculin.
XX Based on the disclosed Mena and Evl genes and proteins, a variety
XX of methods and compositions are provided for screening, isolating
XX and characterizing endogenous and exogenous factors, drugs and
XX therapeutic agents useful to evaluate and/or control cytoskeletal
XX dynamic events involved in normal and abnormal cell morphology,
XX adhesion, motility, growth and/or differentiation. A method of
XX detecting a modulator of Mena activity/expression is claimed.
XX
XX Sequence 1956 BP; 461 A; 571 C; 559 G; 362 T; 3 other;
SQ
Query Match 64.7%; Score 19.4; DB 19; Length 1956;
Best Local Similarity 79.3%; Pred. No. 88;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ctgggcagcaccacgctcggatgcagatc 29
DB 1092 CAGAGCAGCAGCCAGCTGATGCAGAGC 1064
RESULT 42
AAK70210/c
ID AAK70210 standard; DNA; 7885 BP.
XX
XX AAK70210;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:25022.
XX
XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytoskeletal; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
```

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI, 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -


```

CC osteoregulin activity as well as methods of treating mammals for
CC diseases or disorders associated with osteoregulin activity. The
CC modulators of activity may be useful in the manufacture of a
CC medicament for, as well as for treating, a mammal in need of
CC regulation of bone mass and/or density, adiposity, vascular
CC flexibility, and/or atherosclerotic plaque calcification (claimed),
CC for treating and preventing osteoporosis, and for stimulating bone
CC repair and regeneration.
XX
SQ Sequence 1682 BP; 510 A; 401 C; 432 G; 339 T; 0 other;

Query Match      63.3%; Score 19; DB 22; Length 1682;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctggcgacgaccgaagtcgcgatgcaga 27
   ||||| ||||| ||| ||| |||
DB 132 ctggcgacgaccgaatgcgatgaaga 158

RESULT 45
AAQ73500/C
ID AAQ73500 standard; DNA; 8438 BP.
XX
AC AAQ73500;
XX
DF 15-MAY-1995 (first entry)
XX
DE DNA encoding Pseudorabies virus large latency transcript.
XX
KW Pseudorabies virus; PRV; LTV; large latency transcript;
KW attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICP0;
KW protecting animals; deletion mutants; swine; ds.
XX
OS Pseudorabies virus.
XX
FH Key Location/Qualifiers
FT misc_feature 1..7013
   /*tag= a
   /note= "derived from PRV strain Infh"
FT misc_feature 7014..8425
   /*tag= b
   /note= "derived from PRV strain Ka"
FT CDS 622..6498
   /*tag= C
   /note= "encodes predicted amino acid sequence of ORF2"
FT TATA_signal 1..6
   /*tag= d
FT misc_feature 34
   /*tag= e
   /note= "RNA cap site"
FT polyA_signal 8382..8387
   /*tag= f
XX
PN US5352596-A.
XX
PD 04-OCT-1994.
XX
PE 11-SEP-1992; 92US-0945283.
XX
PR 11-SEP-1992; 92US-0945283.
XX
PA (USDA ) US SEC OF AGRIC.
XX
PI Cheung AK, Wesley RD;
XX
DR WPI: 1994-316187/39.
DR P-PSDB; AAR60620.
XX
XX New pseudorabies virus mutants for use in vaccine - having a
PT deletion and/or insertion in the early protein O gene or large
PT latency transcript gene

```

```

XX
PS Disclosure: Column 15-30; 43pp; English.
XX
CC AAQ73500 shows the pseudorabies virus (PRV) large latency transcript
CC (LTV). The basic sequence is derived from PRV strain Infh and PRV
CC strain Ka. The LTV overlaps and is transcribed in the opposite
CC orientation with respect to the EPO (early polypeptide 0) and the
CC immediately early gene (IE180). EPO is nonessential for replicatio,
CC LTR is the only gene expressed during PRV latency, and the IE180
CC gene is absolutely necessary for PRV replication. However there are
CC 2 copies of IE180 in the genome. It is expected that PRV lacking one
CC of the IE180 copies is viable. Deletions in the non-overlapping
CC regions of these 3 genes will generate single deletion routants,
CC while deletions in overlapping regions will generate double deletion
CC mutants. The invention is concerned with the construction of attenuated
CC viruses which have a reduced ability to reactivate from latency. This
CC can be achieved by functionally disabling the expression of the EPO
CC gene, or by disrupting the synthesis of the LTR, or both. (See also
XX AAQ73501 and AAR60620-24)
XX
SQ Sequence 8438 BP; 1141 A; 2916 C; 3327 G; 1054 T; 0 other;

Query Match      63.3%; Score 19; DB 15; Length 8438;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ggcagaccgaagtcgcgatgcagatcc 30
   ||||| ||||| ||| ||| |||
DB 4239 GCCAGCACCAGTCCGCTCCAGCAC 4213

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Search completed: September 10, 2002, 01:51:07
Job time: 436 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 00:37:41 : Search time 45.55 seconds
(without alignments)
161.778 Million cell updates/sec.

Title: US-09-912-436-5_COPY_275_304

Perfect score: 30

Sequence: 1 ctgggcagcaccacacgcgcgatgcgatcc 30

Scoring table: IDENTITY_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 767061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 99%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/prodata/1/lna/CTUS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.8	89.3	405	1	US-08-469-427A-8
2	26.8	89.3	405	2	US-08-609-443B-8
3	26.8	89.3	405	2	US-08-569-063C-8
4	26.8	89.3	565	1	US-08-469-427A-4
5	26.8	89.3	565	2	US-08-609-443B-4
6	26.8	89.3	565	2	US-08-569-063C-4
7	26.8	89.3	624	2	US-08-609-443B-12
8	26.8	89.3	624	2	US-08-569-063C-12
9	26.8	89.3	886	1	US-08-469-427A-1
10	26.8	89.3	886	2	US-08-609-443B-1
11	26.8	89.3	886	2	US-08-569-063C-1
12	23.6	78.7	591	1	US-08-469-427A-6
13	23.6	78.7	591	2	US-08-609-443B-6
14	23.6	78.7	591	2	US-08-569-063C-6
15	19	63.3	8438	1	US-07-945-283-1
16	18.8	62.7	1748	1	US-08-255-471-8
17	18.4	61.3	81	3	US-08-651-136C-73
18	18.4	61.3	4403765	4	US-09-103-840A-2
19	18.4	61.3	4411529	4	US-09-103-840A-1
20	18	60.0	1096	4	US-08-858-207A-136
21	18	60.0	2210	4	US-08-464-700-53
22	18	60.0	2242	1	US-08-641-627A-37
23	18	60.0	2427	2	US-08-678-039A-39
24	17.8	59.3	1338	2	US-08-044-812A-3
25	17.8	59.3	1338	2	US-08-475-637-3
26	17.8	59.3	1338	3	US-08-706-281A-11
27	17.8	59.3	1338	4	US-09-191-359-3

c	28	17.8	59.3	1338	4	US-09-097-231-11	Sequence 11, Appl
c	29	17.6	58.7	2107	1	US-07-795-859B-3	Sequence 3, Appl
c	30	17.6	58.7	2107	1	US-08-457-616-3	Sequence 3, Appl
c	31	17.6	58.7	11873	2	US-08-970-269A-32	Sequence 32, Appl
	32	17.6	58.7	11873	4	US-09-407-562-32	Sequence 32, Appl
	33	17.6	58.7	11878	2	US-08-970-269A-31	Sequence 31, Appl
	34	17.6	58.7	11878	4	US-09-407-562-31	Sequence 31, Appl
	35	17.6	58.7	11883	2	US-08-970-269A-28	Sequence 28, Appl
	36	17.6	58.7	11883	4	US-09-407-562-28	Sequence 28, Appl
	37	17.2	57.3	442	2	US-08-483-528B-53	Sequence 53, Appl
	38	17.2	57.3	442	3	US-08-673-799C-53	Sequence 53, Appl
	39	17.2	57.3	2599	6	5266464-1	Patent No. 5266464
	40	17.2	57.3	4330	3	US-09-310-293-1	Sequence 1, Appl
	41	17.2	57.3	4330	4	US-09-579-376-1	Sequence 1, Appl
	42	17	56.7	1320	2	US-08-641-038A-1	Sequence 1, Appl
	43	17	56.7	1320	2	US-09-059-178-1	Sequence 1, Appl
	44	17	56.7	1369	2	US-08-642-541-1	Sequence 1, Appl
c	45	17	56.7	1369	2	US-08-642-541-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-469-427A-8
: Sequence 8, Application US/08469427A
: Patent No. 5607918
: GENERAL INFORMATION:
: APPLICANT: Eriksson, Ulf
: APPLICANT: Olofsson, Birgitta
: APPLICANT: Alltalo, Karl
: APPLICANT: Pajusola, Katri
: TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
: STREET: 1200 G Street, N.W., Suite 700
: CITY: Washington
: STATE: DC
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,427A
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/397,651
: FILING DATE: 01-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Evans, Joseph D
: REGISTRATION NUMBER: 26,269
: REFERENCE/DOCKET NUMBER: 41979cp2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-8800
: TELEFAX: (202) 628-8844
: INFORMATION FOR SEO ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 405 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-469-427A-8

Query Match 89.3%; Score 26.8; DB 1; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcgagatcc 30
||||| ||||||| |||||||
DB 278 CTGGGCAACACCAAGTCGAGATGCAGATCC 307

RESULT 2

US-08-609-443B-8
; Sequence 8, Application US/08609443B
; Patent No. 5840693

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESS: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
CLASSIFICATION: 435
FILING DATE: 01-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-609-443B-8

Query Match 89.3%; Score 26.8; DB 2; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcgagatcc 30
||||| ||||||| ||||||| |||||||
DB 278 CTGGGCAACACCAAGTCGAGATGCAGATCC 307

RESULT 3
US-08-569-063C-8
; Sequence 8, Application US/08569063C.
; Patent No. 5928939

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-569-063C-8

Query Match 89.3%; Score 26.8; DB 2; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcgagatcc 30
||||| ||||||| ||||||| |||||||
DB 278 CTGGGCAACACCAAGTCGAGATGCAGATCC 307

RESULT 4

US-08-469-427A-4
; Sequence 4, Application US/08469427A
; Patent No. 5607918

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESS: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-4

Query Match 89.3%; Score 26.8; DB 1; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ctgggcagcaccagtcgagtcgagtcgc 30
||||| ||||||| |||||||
Db 273 CTGGGCAACACCAAGTCGGAATCGCATCC 302

RESULT 5
US-08-609-443B-4
Sequence 4, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-609-443B-4

Query Match 89.3%; Score 26.8; DB 2; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ctgggcagcaccagtcgagtcgagtcgc 30
||||| ||||||| |||||||
Db 273 CTGGGCAACACCAAGTCGGAATCGCATCC 302

RESULT 6
US-08-569-063C-4
Sequence 4, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-569-063C-4

Query Match 89.3%; Score 26.8; DB 2; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 273 CTGGGCACACCAAGTCGATGCAGATCC 302

RESULT 7
US-08-609-443B-12
; Sequence 12, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: ALTRIO, Birgitta
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: PAJUSOLA, Kari
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,443B
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/397,651
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA: US 08/469,427
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA: US 08/569,063
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
US-08-609-443B-12

Query Match 89.3%; Score 26.8; DB 2; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.0086;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 CTGGGCACACCAAGTCGATGCAGATCC 304

RESULT 8
US-08-569-063C-12
; Sequence 12, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: ALTRIO, Birgitta
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: PAJUSOLA, Kari
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/569,063C
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA: US 08/469,427
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA: US 08/397,651
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
US-08-569-063C-12

Query Match 89.3%; Score 26.8; DB 2; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.0086;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| |||||||
Db 275 CTGGGCAACACCAAGTCGATGCAGATCC 304

RESULT 9

US-08-469-427A-1
; Sequence 1, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Allitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; IMMEDIATE SOURCE:
; CLONE: pc1f2
; US-08-469-427A-1

Query Match 89.3%; Score 26.8; DB 1; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| |||||||
Db 184 CTGGGCAACACCAAGTCGATGCAGATCC 213

RESULT 10
US-08-609-443B-1
; Sequence 1, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta

; APPLICANT: ALLITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; IMMEDIATE SOURCE:
; CLONE: pc1f2
; US-08-609-443B-1

Query Match 89.3%; Score 26.8; DB 2; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| |||||||
Db 184 CTGGGCAACACCAAGTCGATGCAGATCC 213

RESULT 11
US-08-569-063C-1
; Sequence 1, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALLITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/569,063C
;; FILING DATE: 06-DEC-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/469,427
;; FILING DATE: 06-JUN-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;;
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 886 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: mouse embryo
;; IMMEDIATE SOURCE:
;; CLONE: pc1f2
;;
;; US-08-569-063C-1

Query Match 89.3%; Score 26.8; DB 2; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctggcgacgacccaagtcggatgcagatcc 30
||||| ||||||| ||||||| |||||||

DB 184 CTGGCACAACCAAGTCGATGCAGATCC 213

RESULT 12
US-08-469-427A-6
Sequence 6, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alfalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/469,427A
;; FILING DATE: 06-JUN-1995
;;
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 41979CP2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;;
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 591 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: adult mouse heart
;;
;; US-08-469-427A-6

Query Match 78.7%; Score 23.6; DB 1; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctggcgacgacccaagtcggatgcagatcc 30
||||| ||||||| ||||||| |||||||

DB 278 CTGGCACAACCAAGTCGATGCAGATC 307

RESULT 13
US-08-609-443B-6
Sequence 6, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALFALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-609-443b-6

Query Match 78.7%; Score 23.6; DB 2; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ctgggcagcaccgaatccgatcgagatcc 30
Db 278 CTGGGCAACACCAAGTCGATCGAGGTAC 307

RESULT 14
US-08-569-063c-6
Sequence 6, Application US/08569063c
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Karl
APPLICANT: PAJUSOLA, Karl
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063c
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-569-063c-6

Query Match 78.7%; Score 23.6; DB 2; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ctgggcagcaccgaatccgatcgagatcc 30
Db 278 CTGGGCAACACCAAGTCGATCGAGGTAC 307

RESULT 15
US-07-945-283-1/c
Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EP0 and LIT Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4128
TELEFAX: 309-685-4011 ext.513
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus
FEATURE:
NAME/KEY: CDS
LOCATION: 622..6495
FEATURE:
NAME/KEY: variation
LOCATION: replace(1099, "g")
FEATURE:
NAME/KEY: variation
LOCATION: replace(1267, "t")
FEATURE:

APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 61.3%; Score 18.4; DB 4; Length 4403765;
Best Local Similarity 78.6%; Pred. No. 48;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ttggcagcaccagtcggtgagtcgagtc 29
Db 77236 ttggcagcagatgctggtgagtcgagtc 77263

RESULT 19
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 61.3%; Score 18.4; DB 4; Length 4411529;
Best Local Similarity 78.6%; Pred. No. 48;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ttggcagcaccagtcggtgagtcgagtc 29
Db 77257 ttggcagcagatgctggtgagtcgagtc 77284

RESULT 20
US-08-858-207A-136
Sequence 136, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard

APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-136

Query Match 60.0%; Score 18; DB 4; Length 1096;
Best Local Similarity 80.8%; Pred. No. 50;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ttggcagcaccagtcggtgagtcgagtc 27
Db 1021 TTGGCTGCACCAATCCTGTTGCACA 1046

RESULT 21
US-08-464-700-53/C
Sequence 53, Application US/08464700
Patent No. 6232458
GENERAL INFORMATION:
APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,700
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435

```

1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: AU PL6520
3      FILING DATE: 22-DEC-1992
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: AU PL9661
6      FILING DATE: 28-JUN-1993
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: PCT/AU93/006555
9      FILING DATE: 16-DEC-1993
10     ATTORNEY/AGENT INFORMATION:
11     NAME: Bak, Mary E.
12     REGISTRATION NUMBER: 31,215
13     REFERENCE/DOCKET NUMBER: GHC305A
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 215-540-9200
16     TELEFAX: 215-540-5818
17     INFORMATION FOR SEQ ID NO: 53:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 2210 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23     MOLECULE TYPE: cDNA
24     HYPOTHEetical: NO
25     ANTI-SENSE: NO
26     OS-08-464-700-53

```

Query Match	60.0%	Score 18	DB 4	Length 2210
Best Local Similarity	80.8%	Pred. No. 55		
Matches 21	Conservative 0	Mismatches 5	Indels 0	Gaps 0

Qy	4	g	c	a	c	c	a	a	a	g	t	c	c	g	a	t	c	a	g	a	t	c	29
Db	1577	G	C	C	A	C	C	A	A	G	C	C	C	C	A	G	C	T	G	C	A	G	1552

RESULT 22
 US-08-641-627A-37/C
 Sequence 37 Application US/08641627A
 Patent No. 5726040
 GENERAL INFORMATION:
 APPLICANT: Ensley Phd, Burt D.
 APPLICANT: Ludmer, Matthew
 TITLE OF INVENTION: Cosmetic Compositions Including
 TITLE OF INVENTION: Tropoelastin Isomorphs
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Choate, Hall & Stewart
 STREET: 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: usa
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/641,627A
 FILING DATE: 02-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jarrell Ph.D., Brenda H.
 REGISTRATION NUMBER: 39,223
 REFERENCE/DOCKET NUMBER: 0062912-0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-5000
 TELEFAX: (617) 248-4000
 INFORMATION FOR SEQ ID NO: 37:
 LENGTH: 2242 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; STRAIN: tropoelastin CDNA (CHE-3)
; US-08-641-627A-37

```

Query Match	60.0%	Score 18:	DB 1,	Length 2242;
Best Local Similarity	80.8%	Pred. No. 55;		
Matches 21; Conservative	0;	Mismatches	5;	Gaps 0

QY	4	g	c	a	c	a	c	a	a	a	g	t	c	c	y	a	t	c	a	t	c		29
Db	1714	G	C	A	G	C	A	C	C	A	G	C	C	A	G	T	G	C	A	G	C	T	1689

```

RESULT 23
US-08-678-039A-39/C
: Sequence 39. Application US/08678039A
: Patent No. 5858662
:
: GENERAL INFORMATION:
:
: APPLICANT: Keating, Mark T.
: APPLICANT: Morris, Colleen A.
: TITLE OF INVENTION: Diagnosis of Williams Syndrome and
: TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
: TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene

```

```

1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: Patent Release #1.0, Version #1.30
6      CURRENT APPLICATION DATA:
7      APPLICATION NUMBER: US/08/678,039A
8      FILING DATE: 10-JUL-1996
9      CLASSIFICATION: 435
10     ATTORNEY/AGENT INFORMATION:
11     NAME: Saxe, Stephen A.
12     REGISTRATION NUMBER: 38,609
13     REFERENCE/DOCKET NUMBER: 2323-120A
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 202-624-1589
16     TELEFAX: 202-783-6031
17     INFORMATION FOR SEQ ID NO: 39:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 2427 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23     MOLECULE TYPE: cDNA
24     HYPOTHETICAL: NO
25     ANTI-SENSE: NO
26     ORIGINAL SOURCE:
27     ORGANISM: Homo sapiens
28     FEATURE:
29     NAME/KEY: CDS
30     LOCATION: 49..2424
31     OS-08-678-039A-39

```

Query Match	60.0%	Score 18	DB 2	Length 2427
Best Local Similarity	80.8%	Pred. No.	56	
Matches 21	Conservative	0	Mismatches	5
			Indels	0
			Gaps	0

QY 4 ggcagcaccagtcgcgatgcagatc 29
| | | | | | | | | | | | | | | | |
DB 1800 GCCAGCACCAGCCAGCTGCAGCTC 1775

RESULT 24
US-08-044-812A-3/c
; Sequence 3, Application US/08044812A
; Patent No. 5817521

GENERAL INFORMATION:

APPLICANT: Cone, Roger D
APPLICANT: Roselli-Rehuss, Linda
APPLICANT: Mountjoy, Kathleen G

APPLICANT: Robbins, Linda S

TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone

TITLE OF INVENTION: Receptors and Uses

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,812A

FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 5837521nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,835

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..297

FEATURE:

NAME/KEY: CDS

LOCATION: 298..1269

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 1270..1338

US-08-044-812A-3

Query Match 59.3%; Score 17.8; DB 2; Length 1338;
Best Local Similarity 75.9%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 tgggcagcaccagtcgcgatgcagatc 30
| | | | | | | | | | | | | | | | |
DB 292 TCGGCGGAGCAGTTCGCGCTGCAGCTCC 264

RESULT 25

US-08-475-637-3/c
; Sequence 3, Application US/08475637

Patent No. 5994087

GENERAL INFORMATION:

APPLICANT: Cone, Roger D

APPLICANT: Roselli-Rehuss, Linda

APPLICANT: Mountjoy, Kathleen G

APPLICANT: Robbins, Linda S

TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone

TITLE OF INVENTION: Receptors and Uses

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,637

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,812

FILING DATE: 04-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 5994087nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,835

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..297

FEATURE:

NAME/KEY: CDS

LOCATION: 298..1269

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 1270..1338

US-08-475-637-3

Query Match 59.3%; Score 17.8; DB 2; Length 1338;
Best Local Similarity 75.9%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 tgggcagcaccagtcgcgatgcagatc 30
| | | | | | | | | | | | | | | | |
DB 292 TCGGCGGAGCAGTTCGCGCTGCAGCTCC 264

RESULT 26

US-08-706-281A-11/c
; Sequence 11, Application US/08706281A
; Patent No. 6100048

GENERAL INFORMATION:

APPLICANT: Cone, Roger D

APPLICANT: Fan, Wei

APPLICANT: Boston, Bruce A

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..297
FEATURE:
NAME/KEY: CDS
LOCATION: 298..1269
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1270..1338
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-097-231-11

Query Match 59.3%; Score 17.8; DB 4; Length 1338;
Best Local Similarity 75.9%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 ttgggcagcaccagtcgcgatgc 30
||||| ||||| ||||| ||||| |||||
Db 292 TCGGCGGACCAAGTCCGCGTCGACATCC 264

RESULT 29
US-07-795-859B-3/C
Sequence 3, Application US/07795859B
Patent No. 5422262
GENERAL INFORMATION:
APPLICANT: Anderson, Stefan
APPLICANT: Russell, David W.
TITLE OF INVENTION: Steroid 5 α -Reductases
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P O Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/795,859B
FILING DATE: 18-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:260/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7677
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 31..807
US-07-795-859B-3

Query Match 58.7%; Score 17.6; DB 1; Length 2107;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatgc 24
||||| | ||||| |||||
Db 1430 CTGGCGTGGAACAAGTCCGATGC 1407

RESULT 30
US-08-457-616-3/C
Sequence 3, Application US/08457616
Patent No. 5679521
GENERAL INFORMATION:
APPLICANT: Anderson, Stefan
APPLICANT: Russell, David W.
TITLE OF INVENTION: Steroid 5 α -Reductases
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P O Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,616
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/795,859
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:260/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7677
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 31..807
US-08-457-616-3


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; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970_269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
;
US-08-970-269A-31

Query Match 58.7%; Score 17.6; DB 2; Length 11878;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 gcacaccaagtcgcgatcgat 28
||||| ||||| ||||| |||||
Db 5519 GCACGACGACGATGGGATTCAGAT 5542

RESULT 34
US-09-407-562-31
; Sequence 31, Application US/09407562
; Patent No. 6294334
; GENERAL INFORMATION:
; APPLICANT: Kathryn Weck
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: No. 6294334ember 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
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```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
;
US-09-407-562-31

Query Match 58.7%; Score 17.6; DB 4; Length 11878;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 gcacaccaagtcgcgatcgat 28
||||| ||||| ||||| |||||
Db 5519 GCACGACGACGATGGGATTCAGAT 5542

RESULT 35
US-08-970-269A-28
; Sequence 28, Application US/08970269A
; Patent No. 5976803
; GENERAL INFORMATION:
; APPLICANT: Kathryn Weck
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11883 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
;
US-08-970-269A-28

Query Match 58.7%; Score 17.6; DB 2; Length 11883;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 5 gcagcaccgaagtcggatgcagat 28
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Db 5521 GCAGCAGCAAGTGGGATTCAGAT 5544

RESULT 36
US-09-407-562-28

; Sequence 28, Application US/09407562
; Patent No. 6294334

; GENERAL INFORMATION:

; APPLICANT: Kathryn Meek

; TITLE OF INVENTION: Genetic Test For Equine Severe

; TITLE OF INVENTION: Combined Immunodeficiency Disease

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Benjamin A. Adler

; STREET: 8011 Candle Lane

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Macintosh

; SOFTWARE: Microsoft Word for Macintosh

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/407,562

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/970,269

; FILING DATE: No. 6294334ember 14, 1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler Ph.D., Benjamin A.

; REGISTRATION NUMBER: 35,423

; REFERENCE/DOCKET NUMBER: D5860

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-777-2321

; TELEFAX: 713-777-6908

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11883 bp

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: other nucleic acid

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; US-09-407-562-28

; Query Match 58.7%; Score 17.6; DB 4; Length 11883;

; Best Local Similarity 83.3%; Pred. No. 1e+02;

; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 gcagcaccgaagtcggatgcagat 28
||||| ||||| ||||| |||||

Db 5521 GCAGCAGCAAGTGGGATTCAGAT 5544

RESULT 37
US-08-483-528B-53

; Sequence 53, Application US/08483528B

; Patent No. 5939532

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,528B

; FILING DATE: 07-JUN-95

; CLASSIFICATION: 536

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4100

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "synthetic DNA"

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens and mouse

; FEATURE:

; NAME/KEY: sig-peptide

; LOCATION: -15..-1

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; FEATURE:

; NAME/KEY: domain

; LOCATION: 31..35

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR1"

; FEATURE:

; NAME/KEY: domain

; LOCATION: 50..66

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR2"

; FEATURE:

; NAME/KEY: domain

; LOCATION: 99..109

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR3"

; US-08-483-528B-53

; Query Match 57.3%; Score 17.2; DB 2; Length 442;

; Best Local Similarity 73.3%; Pred. No. 95;

; Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaagtcggatgcagatc 30
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Db 124 CTGACCTGCACCGTGTCCGATACACATTC 153

RESULT 38
US-08-673-799C-53

; Sequence 53, Application US/08673799C

; Patent No. 6042828

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,799C
FILING DATE: 27-JUN-96
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens and mouse
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -19...-1
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
FEATURE:
NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR1"
FEATURE:
NAME/KEY: domain
LOCATION: 50..66
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR2"
FEATURE:
NAME/KEY: domain
LOCATION: 99..109
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR3"
US-08-673-799C-53

Query Match 57.3%; Score 17.2; DB 3; Length 442;
Best Local Similarity 73.3%; Pred. No. 95;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ctggcgacgacccaagtcgcgatgcagatcc 30
||| | |||| | |||| | ||| |
Db 124 ctgacctgcacccgtctccgatatcacatttc 153

RESULT 39
5266464-1
; Patent No. 5266464
; APPLICANT: HOUSEY, GERRARD
; TITLE OF INVENTION: METHOD OF SCREENING FOR PROTEIN INHIBITORS
; AND ACTIVATORS
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,073

FILING DATE: 10-AUG-16989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 154,206
FILING DATE: 10-FEB-1988
SEQ ID NO:1:
LENGTH: 2599
5266464-1

Query Match 57.3%; Score 17.2; DB 6; Length 2599;
Best Local Similarity 73.3%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ctggcgacgacccaagtcgcgatgcagatcc 30
||| | |||| | |||| | ||| |
Db 1281 ctgggaagcccccattccgtactcagatcc 1310

RESULT 40
US-09-310-293-1
; Sequence 1, Application US/09310293
; Patent No. 6117662
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Traini, Christopher M.
; APPLICANT: Mathie, Thomas B.
; TITLE OF INVENTION: Respiratory nitrate reductase alpha
; FILE REFERENCE: GM10000
; CURRENT APPLICATION NUMBER: US/09/310,293
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/086,579
; EARLIER FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4330
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-310-293-1

Query Match 57.3%; Score 17.2; DB 3; Length 4330;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ctggcgacgacccaagtcgcgatgcagatcc 30
||| | |||| | |||| | ||| |
Db 1328 ctggctacgacccgaatccgtgtccagatgc 1357

RESULT 41
US-09-579-376-1
; Sequence 1, Application US/09579376
; Patent No. 6316237
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Traini, Christopher M.
; APPLICANT: Mathie, Thomas B.
; TITLE OF INVENTION: Respiratory nitrate reductase alpha
; FILE REFERENCE: GM10000
; CURRENT APPLICATION NUMBER: US/09/579,376
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/310,293
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/086,579
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

LENGTH: 4330
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-579-376-1

Query Match 57.3%; Score 17.2; DB 4; Length 4330;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ctggcgacgaccgaagtcgcgatgcagatcc 30
||||| ||||| ||||| ||||| ||||| |||||
Db 1328 ctggcgacgaccgaagtcgcgatgcagatcc 1357

RESULT 42
US-08-641-038A-1
Sequence 1, Application US/08641038A
Patent No. 5861154
GENERAL INFORMATION:

APPLICANT: SODA, KENJI
APPLICANT: TANAKA, HIDEHIKO
APPLICANT: INOUE, HIROYUKI
APPLICANT: INAGAKI, KENJI
APPLICANT: ESAKI, NOBUYOSHI
TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA

COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,038A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020-3989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:

NAME/KEY: CDS
LOCATION: 61..1254
US-08-641-038A-1

Query Match 56.7%; Score 17; DB 2; Length 1320;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctggcgacgaccgaagtcgcgatgca 25
||||| ||||| ||||| ||||| ||||| |||||
Db 385 CTGGCGACACCGCTGTACGGCTGCA 409

RESULT 43

US-09-059-178-1
Sequence 1, Application US/09059178
Patent No. 5863788
GENERAL INFORMATION:

APPLICANT: SODA, KENJI
APPLICANT: TANAKA, HIDEHIKO
APPLICANT: INOUE, HIROYUKI
APPLICANT: INAGAKI, KENJI
APPLICANT: ESAKI, NOBUYOSHI
TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA

COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,178
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/641,038
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020-3989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:

NAME/KEY: CDS
LOCATION: 61..1254
US-09-059-178-1

Query Match 56.7%; Score 17; DB 2; Length 1320;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctggcgacgaccgaagtcgcgatgca 25
||||| ||||| ||||| ||||| ||||| |||||
Db 385 CTGGCGACACCGCTGTACGGCTGCA 409

RESULT 44
US-08-642-541-1
Sequence 1, Application US/08642541
Patent No. 5891704
GENERAL INFORMATION:

APPLICANT: YUYING, TAN
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCED
THEREFROM AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,541
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Millman, Robert A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 31276-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1241
US-08-642-541-1

Query Match 56.7%; Score 17; DB 2; Length 1369;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgca 25
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Db 372 ctgggcacacccctgtagcgtgca 396

RESULT 45
US-08-642-541-3/C
Sequence 3, Application US/08642541
Patent No. 5891704
GENERAL INFORMATION:
APPLICANT: YUYING, TAN
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
TITLE OF INVENTION: METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,541
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Millman, Robert A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 31276-20002.21
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: YES
ANTI-SENSE: YES
US-08-642-541-3

Query Match 56.7%; Score 17; DB 2; Length 1369;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgca 25
|||||
Db 998 ctgggcacacccctgtagcgtgca 974

Search completed: September 10, 2002, 01:51:28
Job time: 4427 sec

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/clone_1b="Canis CNAs from mdck cells"
/notes="vector: Lambda zap II; The library was provided by
Greg Hannon (Cold Spring Harbor Laboratory). This
library is oligo(dT) primed using strataene zap cna
synthesis kit. It was made from exponentially growing mdck

```

cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT 65 a 138 c 132 g 68 t 2 others

ORIGIN

Query Match 94.7%; Score 28.4; DB 9; Length 405;
Best Local Similarity 96.7%; Pred. No. 1;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagaccagtcgcgatcgatcc 30
|||||
DB 329 CTGGGCAGCACCAGTCCGATGCAGATCC 358

RESULT 2
LOCUS AL529876 935 bp mRNA linear EST 13-FEB-2001
DEFINITION AL529876 LTI_NFL001_NBC4 Homo sapiens CDNA clone CS0DD005YH10 5
prime, mRNA sequence.
ACCESSION AL529876
VERSION AL529876.1 GI:12793369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 935)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source Location/Qualifiers

1..935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD005YH10"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 182 a 319 c 287 g 141 t 6 others
ORIGIN

Query Match 94.7%; Score 28.4; DB 9; Length 935;
Best Local Similarity 96.7%; Pred. No. 1.1;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagaccagtcgcgatcgatcc 30
|||||
DB 413 CTGGGCAGCACCAGTCCGATGCAGATCC 442

RESULT 3
LOCUS BE297480 699 bp mRNA linear EST 20-JUL-2000
DEFINITION 601176041F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:3531179 5',
mRNA sequence.
ACCESSION BE297480

VERSION BE297480.1 GI:9181160
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 699)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM205 row: b column: 12
High quality sequence start: 35
High quality sequence stop: 657.

FEATURES
Source Location/Qualifiers

1..699
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3531179"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 130 a 247 c 201 g 121 t
ORIGIN

Query Match 91.3%; Score 27.4; DB 10; Length 699;
Best Local Similarity 96.6%; Pred. No. 2.5;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagaccagtcgcgatcgatcc 29
|||||
DB 202 CTGGGCAGCACCAGTCCGATGCAGATCC 230

RESULT 4
LOCUS AA434485 531 bp mRNA linear EST 29-MAY-1997
DEFINITION zw31a04.r1 Soares ovary tumor NBH07 Homo sapiens CDNA clone IMAGE:770862 5', similar to TR:G1216398 G1216398 VEGF RELATED FACTOR ISOFORM VRF167 PRECURSOR. ;, mRNA sequence.
ACCESSION AA434485
VERSION AA434485.1 GI:2139399
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 531)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maita, M., Martin, T., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.

TITLE Mashu-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: estevenson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amerasham
High quality sequence stop: 470.

FEATURES
Source

1.531
/organism="Homo sapiens"
/db_xref="GDB:5980735"
/db_xref="taxon:9606"
/clone="IMAGE:770862"
/clone.lib="Soares ovary tumor NBH09"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pRT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
'GCTTACCATCTGAGTGGAGCGCCGCTTTTCTTTTCTTTT 3')
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 111 a 162 c 163 g 95 t

ORIGIN

Query Match 90.0%; Score 27; DB 9; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggcagcaccagtcgcgatgcagatcc 30
|||||
Db 191 GGCAGCACCAAGTCCGATGCAGATCC 217

RESULT 5
BF582738 799 bp mRNA linear EST 12-DEC-2000
LOCUS 602094158F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208222 5',
DEFINITION mRNA sequence.
ACCESSION BF582738
VERSION BF582738.1 GI:11656456
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM9772 row: d column: 15
High quality sequence stop: 711.
Location/Qualifiers

FEATURES
Source

1.799
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208222"
/clone.lib="NCI_CGAP_Co24"

/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPOrt6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 210 a 241 c 203 g 145 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 799;
Best Local Similarity 93.3%; Pred. No. 4.2;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacagtcgcgatgcagatcc 30
|||||
Db 61 CTGGCGACACCAAGTCCGATGCAGATCC 90

RESULT 6
BM007641 919 bp mRNA linear EST 30-OCT-2001
LOCUS 603617063F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:3441079 5',
DEFINITION mRNA sequence.
ACCESSION BM007641
VERSION BM007641.1 GI:16521995
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1914 row: m column: 16
High quality sequence stop: 669.
Location/Qualifiers

FEATURES
Source

1.919
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5441079"
/clone.lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOMB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 179 a 230 c 326 g 182 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 919;
Best Local Similarity 93.3%; Pred. No. 4.3;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacagtcgcgatgcagatcc 30
|||||
Db 129 CTGGCGACACCAAGTCCGATGCAGATCC 158

[illegible]

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	1 (bases 1 to 685)
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNI at: http://image.llnl.gov Plate: LAM11449 row: p column: 17 High quality sequence stop: 402. Location/Qualifiers 1..685 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5180416" /clone_lib="NIH_MGC_115" /lab_host="DH10B" /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
BASE COUNT	182 a 232 c 178 g 93 t
ORIGIN	
Query Match	86.7%; Score 26; DB 10; Length 685;
Best Local Similarity	100.0%; Pred. NO. 8.2;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GCAGCACCACAGTCGCGATGCAGATCC 26
QY	5 gcagcaccacagtcgcgagtcagatcc 30
RESULT 9	
BB374531	
LOCUS	BB374531 266 bp mRNA linear EST 13-JUL-2000
DEFINITION	musculus cDNA clone C130075112 3' similar to AF032925 Rattus noveboracensis vascular endothelial growth factor B 186 precursor, mRNA sequence.
ACCESSION	BB374531
VERSION	BB374531.1 GI:9087025
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 266) Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Horii,F., Ishii,Y., Ishikawa,U., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Taya

TITLE
JOURNAL
COMMENT

Y., Tsunoda, Y., Watahiki, A., Matanabe, S., Yamamura, T., Yamanaka, I.,
'Tano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiaki, A., Yoshino
'M., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshinhide Hayashizaki

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenryo-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: <http://genome.qsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasakawa,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotranscription and the reactivation of thermophilic enzymes by
thymine and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Katsunuma, T., Akiyama, J., Shibata, K., Itawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.irc.riken.go.jp/>) for
further details.

FEATURES

Location/Qualifiers
1. .266

```

source
1..266
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C13007S112"
/clone_id="RIKEN full-length enriched, 16 days embryo
head"
sex="mixed"
/tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGGAGAGAAGATCCCAAGACCTCTTTTCTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adaptor of sequence [5',
GAGGAGAGATCTTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified plusscript KS(+) after bulk excision from Lambda
PLC I"
```

Query Match	78.7%;	Score 23.6;	DB 9;	Length 266;
Best Local Similarity	86.7%;	Pred. No. 55;		
Matches	26; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;

```

QY      1 ctggcgagcaccacaagtcgcgatgcagatcc 30
        ||| ||| ||| ||| ||| ||| ||| |||
Db      163 CTGCGCAACACCAATTCGGAATGCAGATCC 192

```

RESULT 10	555 bp	DNA	linear	GSS 29-SEP-2000
AZ341037/c				
LOCUS				
AZ341037				

DEFINITION	1M0073B15F Mouse 10kb plasmid U0GC1M library Mus musculus genomic clone U0GC1M0073B15 F, DNA sequence.
ACCESSION	AF341037
VERSION	AF341037.1
KEYWORDS	GI:10416888
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus.

REFERENCE AUTHORS

TITLE	Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts
FILE	mouse_scaffolding.plasmid_inserts

JOURNAL
COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: B column: 15
Seq primer: CCGTGTAAACGACGCCCACT
Class: plasmid ends
High quality sequence step: 555.

FEATURES
source

Location/Qualifiers
1. .555

```

BASE COUNT
ORIGIN
132 a 173 c 138 g 112 t

/origins:sm="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="WUCG1M0073B15"
/clone_lib="Mouse 10kb plasmid WUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match	78.7%;	Score 23.6;	DB 12;	Length 555;
Best Local Similarity	86.7%;	Pred. No. 60;		
Matches 26; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      1  ctgggcagcaccacgaatccggaatgcagatcc 30
          |||||  |||||  |||||  |||||  |
Db      451  CTGGGCAACACCAAGTCCGAATGCAGGTAC 422
```

RESULT 11
AA073660

LOCUS	AA073660	423 bp	MRNA	linear	EST 15-FEB-1997
DEFINITION	mm4g9606.r1 Striatogene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536122 5' similar to TR:G1314336 G1314336 M9F167. ;, mRNA sequence.				
ACCESSION	AA073660.1	GI:1595394			
VERSION	AA073660				
KEYWORDS	EST.				
ORGANISM	house mouse.				
SOURCE	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 423)				
AUTHORS	Marra, S., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gessel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Weisberg, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.				
TITLE	The WashU-HHMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contract: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMC Consortium (info@image.lnl.gov) for further information. MGI:323058 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 411. Location/Qualifiers 1..423 /organism="Mus musculus" /strain="NIH/Swiss" /db_xref="taxon:10090" /clone="IMAGE:536122" /clone_lib="Striatogene mouse heart (#937316)" /sex="pooled" /tissue="type="heart" /dev_stage="13 day embryos" /lab_host="SOLR (kanamycin resistant)" /note="Organ: heart; Vector: plasmidscript SK-; Site_1: Ecot1; Site_2: Xho1; Cloned unidirectionally. Primer: 0150 dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"				
BASE COUNT	96 a	135 c	123 g	69 t	
ORIGIN					
Query Match	74.0%;	Score 22.2;	DB 9;	Length 423;	
Best Local Similarity	88.9%;	Pred. No.1.9e+02;			
Matches 24;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	4	ggcagcaccacgaagtcgcgattcgagatcc 30			
Db	52	GGGACACCAAGTCGCAATGCAGATCC 78			
RESULT 12					
BI087310	BI087310	579 bp	MRNA	linear	EST 20-JUN-2001
LOCUS	602850965f1 NIH_MGC_10	Homo sapiens	CDNA clone	IMAGE:4992305 5',	
DEFINITION	mRNA sequence.				
ACCESSION	BI087310	GI:14505640			
VERSION	BI087310.1	GI:14505640			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				

REFERENCE	1 (bases 1 to 579)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@b3.rnemail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov plate: LHAM1011 row: b column: 18 High quality sequence stop: 579. Location/Qualifiers
FEATURES	1..579
source	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4992305" /clone_id="NIH_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI; Site-2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT	123 a 211 c 154 g 91 t
ORIGIN	
Query Match	70.0%; Score 21; DB 10; Length 579;
Best Local Similarity	100.0%; Prid. No. 5,4e+02;
Matches	21; Conservatvity 0; Mismatches 0; Indels 0; Gaps 0;
Oy	10 accaaagtcgcatgcagatcc 30
Db	22 ACCAAGTCGCGATGCAGATCC 42
RESULT 13	
LOCUS	A1174183 389 bp mRNA linear EST 07-OCT-1998
DEFINITION	uc07b07.f1 Soares_mammary_gland_NbMG Mus musculus cDNA clone IMAGE:1391269 5' similar to SW:VGBG_MOUSE_P49766 VASCULAR ENOTHELIAL GROWTH FACTOR B PRECURSOR ; , mRNA sequence.
ACCESSION	A1174183
VERSION	A1174183.1 GI:3720325
KEYWORDS	EST.
SOURCE	house mouse. Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 389) Matra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucada,T., Lacy,M., Le,M., Martin,U., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Teisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
AUTHORS	The WashU-HMI Mouse EST project Unpublished (1996) Contact: Matra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNLN, contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:908985
TITLE	Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 378.
JOURNAL	
COMMENT	

	FEATURES	
	SOURCE	Location/Qualifiers 1..389 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /cclone="IMAGE:1397269" /clone_lib="Soares_mammary_gland_NbmMG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5', TGTACCAATCTGAGTCGGAGCGCCGCAGATGTTTTTTTTTTTTTTT TT 3']); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Patima BonaldO."
	BASE COUNT	89 a 105 c 117 g 78 t
	ORIGIN	
Oy	Query Match	69.3%; Score 20.8; DB 9; Length 389;
	Best Local Similarity	91.7%; Pred. No. 6.1e+02;
	Matches 22; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Dd	7 agcaccaagtcgcgatgcatcc 30 Db 270 AACACCAGAATCCGAATGCAGATCC 293	
RESULT 14		
BES43967	LOCUS	BES43967 620 bp mRNA linear EST_09-AUG-2000
	DEFINITION	601070480F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3456642 5' ,
	ACCESSION	mRNA sequence.
	VERSION	BES43967
	KEYWORDS	BES43967.1 GI:972612
SOURCE		EST.
ORGANISM		human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 620) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: ATCC CDNA library Preparation: Life Technologies, Inc. CDNA library Arrayed by: Incyte Genomics, Inc. DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov plate: LAM8444 row: P column: 19 High quality sequence stop: 620.
COMMENT	JOURNAL	Location/Qualifiers 1..620 /organism="Homo saplens" /db_xref="taxon:9606" /cclone="IMAGE:3456642" /clone_lib="NH_MGC_12" /tissue_type="cervical carcinoma cell line" /lab_host="DH10B" /note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
FEATURES		
SOURCE		

[illegible]

DEFINITION 601111886f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352484 5', mRNA sequence.

ACCESSION BE254933

VERSION BE254933.1 GI:9125366

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS 1 (bases 1 to 783)

TITLE NIH-MGC http://mhc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM151 row: 1 column: 21
High quality sequence stop: 665.

FEATURES
source
Location/Qualifiers
1..783
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3352484"
/clone_1lb="NIH_MGC_16"
/tissue_type="Telinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOT87; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 125 a 273 c 242 g 143 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 783;
Best Local Similarity 85.2%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaatcgatcgatcc 30
|||||
Db 341 GGCAGCACCATGCTCTCATGAGATCC 367

RESULT 17
BE547100 793 bp mRNA linear EST 09-AUG-2000
LOCUS 601072507f1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458856 5', mRNA sequence.

ACCESSION BE547100

VERSION BE547100.1 GI:9775665

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS 1 (bases 1 to 793)

TITLE NIH-MGC http://mhc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1AM8450 row: m column: 01
High quality sequence stop: 639.

FEATURES
source
Location/Qualifiers
1..793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3458856"
/clone_1lb="NIH_MGC_12"
/tissue_type="Cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

BASE COUNT 139 a 273 c 239 g 142 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 793;
Best Local Similarity 85.2%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaatcgatcgatcc 30
|||||
Db 152 GGCAGCACCATGCTCTCATGAGATCC 178

RESULT 18
BF345759 828 bp mRNA linear EST 22-NOV-2000
LOCUS 602017820f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153397 5', mRNA sequence.

ACCESSION BF345759

VERSION BF345759.1 GI:11293354

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS 1 (bases 1 to 828)

TITLE NIH-MGC http://mhc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1AM9421 row: h column: 06
High quality sequence stop: 766.

FEATURES
source
Location/Qualifiers
1..828
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4153397"
/clone_1lb="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: PCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 147 a 266 c 265 g 150 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 828;
 Best Local Similarity 85.2%; Pred. No. 8e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatcgcatgcagatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 473 GGCAGCACCATGCTCTCATGAGATCC 499

RESULT 19
 BF984155 1131 bp mRNA linear EST 23-JAN-2001
 DEFINITION 602306859F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397966 5',
 mRNA sequence.
 ACCESSION BF984155
 VERSION BF984155.1 GI:12386967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1131)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LHAM10099 row: f column: 15
 High quality sequence stop: 720.

FEATURES
 source Location/Qualifiers
 1..1131
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4397966"
 /clone_1lb="NIH-MGC_88"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: small intestine; Vector: PCMV-SPORT6;
 Site.1: NotI; Site.2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 265 a 358 c 318 g 190 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 1131;
 Best Local Similarity 85.2%; Pred. No. 8.3e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatcgcatgcagatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 378 GGCAGCACCATGCTCTCATGAGATCC 404

RESULT 20
 A2026632 565 bp DNA linear GSS 25-FEB-2000
 LOCUS A2026632
 DEFINITION RPCI-23-345P3.J1 RPCI-23 Mus musculus genomic clone RPCI-23-345P3,
 DNA sequence.
 ACCESSION A2026632
 VERSION A2026632.1 GI:7102016
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Zhao, S., Niernman, W., Feldblyum, T., Malek, V., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Teegye, G., Geer, K., Kroll, M., de Jong, P.
 and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other-GSSs: RPCI-23-345P3.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (inforesgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 345 row: P column: 3
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..565
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-345P3"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site.1:
 EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Site
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 120 a 149 c 180 g 115 t

ORIGIN

Query Match 68.0%; Score 20.4; DB 12; Length 565;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ctggcagcaccgaatcgcatgcagatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 369 CTGGCAGCACCAACGACTGCTGCAGAGAC 340

RESULT 21
 BM008260 851 bp mRNA linear EST 30-OCT-2001
 LOCUS BM008260
 DEFINITION 603616890F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440486 5',
 mRNA sequence.
 ACCESSION BM008260
 VERSION BM008260.1 GI:16522614
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 851)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov

Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CMI913 row: d column: 23
High quality sequence stop: 699.

FEATURES

Location/Qualifiers

1. 851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5440486"
/clone_1lb="NIH.MGC.113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH.MGC Library."

BASE COUNT 233 a 219 c 244 g 154 t 1 others
ORIGIN

Query Match 68.0%; Score 20.4; DB 10; Length 851;
Best Local Similarity 80.0%; Pred. No. 9.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 cttggcagcagcaagtcggatcgacatcc 30
|||||
Db 537 CTGGCAGCAGCAGGTTCACATGCAGTCCC 508

RESULT 22 336 bp mRNA linear EST 10-MAY-2001
LOCUS AM829906
DEFINITION ra47c11.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
ACCESSION CDNA 5', mRNA sequence.
VERSION AM829906
KEYWORDS AM829906.1 GI:7923720
SOURCE EST.
ORGANISM southern root-knot nematode.
Eukaryota; Metazoa; Chordata; Tylenchida; Tylenchina; Tylenchoidea; Heterodera; Meloidogyinae; Meloidogyne.

REFERENCE 1 (bases 1 to 336)
AUTHORS McCarter,J., Clifton,S., Chapell,B., Pape,D., Martin,J., Wylie,T., Dente,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shiu,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
The library was constructed by Uma Rao and David Bird (david.dird@ncsu.edu) at North Carolina State University. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.

Seq primer: -40RP from Gibco
High quality sequence stop: 327.
Location/Qualifiers

source

1. 336
/organism="Meloidogyne incognita"
/db_xref="taxon:6306"
/clone_1lb="Bird-Rao Meloidogyne incognita J2"
/dev_stage="enriched for 2nd stage juveniles"
/lab_host="X10RL"
/note="Vector: ZAP express - PBKCMV (Stratagene); Site_1: EcoRI; Site_2: XhoI; Oligo (dT) primed library. CDNA was constructed and cloned unidirectionally into the vector within the 5' EcoRI and 3' XhoI sites. This library was constructed by Dr. Uma Rao and Dr. David Bird at North Carolina state University."

BASE COUNT 114 a 50 c 60 g 112 t
ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 gggcagcagcaagtcggatcgacatcc 30
|||||
Db 214 GGGCAGCTCCAGTCCGCTGCGCC 187

RESULT 23 369 bp mRNA linear EST 25-SEP-1997
LOCUS AA594466
DEFINITION n194d03.s1 NCI_CGAP_Co10 Homo sapiens CDNA clone IMAGE:1058309 3', mRNA sequence.
ACCESSION AA594466
VERSION AA594466.1 GI:2409816
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbfp/image/image.html
Insert Length: 1458 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 333.
Location/Qualifiers

FEATURES

source

1. 369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1058309"
/clone_1lb="NCI_CGAP_Co10"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares)."

BASE COUNT 68 a 98 c 112 g 91 t
ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 369;
 Best Local Similarity 82.1%; Pred. No. 1.2e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 gggcagaccacgaatccgagatcgacatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 135 GGGCGCCACTAAGTCGACGACGATCC 162

RESULT 24
 BE578204 407 bp mRNA linear EST 10-MAY-2001
 LOCUS BE578204/c
 DEFINITION rK09b07.y1 Meloidogyne javanica Egg SL1 Topol Kioek Chiapelli
 McCarter Meloidogyne javanica cDNA 5', mRNA sequence.
 BE578204
 BE578204.1 GI:9629146
 VERSION BE578204
 KEYWORDS EST.
 SOURCE root-knot nematode.
 ORGANISM Meloidogyne javanica
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
 1 (bases 1 to 407)
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshill,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 , M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 CONTACT: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Andrew Kioek
 (kioek@biology.wustl.edu) at Divergence LLC, and Brandt Chiapelli
 (bchiapeli@watson.wustl.edu) and Dr. Jim McCarter
 (jmcarter@watson.wustl.edu) at Washington University Genome
 Sequencing Center. DNA Sequencing by: Washington University Genome
 Sequencing Center St. Louis.
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1. 407
 /organism="Meloidogyne javanica"
 /db_xref="taxon:6303"
 /clone_lib="Meloidogyne javanica Egg SL1 Topol Kioek
 Chiapelli McCarter"
 /dev_stage="enriched for eggs"
 /lab_host="DH10B"
 /note="Vector: pCRII-TOPO. SL1-Oligo(dT) PCR-based
 library. Meloidogyne javanica cDNA PCR products of size
 approximately 600-1200 nucleotides containing SL1 on the
 5' end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO (Invitrogen) following the Topo TA
 cloning protocol. cDNA products were size separated. The
 cDNA insert can be excised by digestion with EcoRI. The
 library was constructed by Dr. Andrew Kioek at Divergence
 LLC and Brandt Chiapelli and Dr. James McCarter at
 Washington University, St. Louis. Nematodes were provided
 by Dr. David Bird of North Carolina State University."

BASE COUNT 148 a 62 c 66 g 131 t

ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 407;
 Best Local Similarity 82.1%; Pred. No. 1.2e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 gggcagaccacgaatccgagatcgacatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 199 GGGCAGCTCCAACTCCGGCGCTGCGCC 172

RESULT 25
 AM829955 437 bp mRNA linear EST 10-MAY-2001
 LOCUS AM829955/c
 DEFINITION ra4Bc04.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
 cDNA 5', mRNA sequence.
 CDNA 5', mRNA sequence.
 AM829955
 AM829955.1 GI:7923770
 VERSION AM829955
 KEYWORDS EST.
 SOURCE southern root-knot nematode.
 ORGANISM Meloidogyne incognita
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
 1 (bases 1 to 437)
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshill,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 , M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 CONTACT: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Uma Rao and David Bird
 (david.bird@ncsu.edu) at North Carolina State University. DNA
 Sequencing by: Washington University Genome Sequencing Center St.
 Louis.
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1. 437
 /organism="Meloidogyne incognita"
 /db_xref="taxon:6306"
 /clone_lib="Bird-Rao Meloidogyne incognita J2"
 /dev_stage="enriched for 2nd stage juveniles"
 /lab_host="XLOLR"
 /note="Vector: ZAP express - PBKCMV (Stratagene); Site.1:
 EcoRI; Site.2: XhoI; Oligo (dT) primed library. cDNA was
 constructed and cloned unidirectionally into the vector
 within the 5' EcoRI and 3' XhoI sites. This library was
 constructed by Dr. Uma Rao and Dr. David Bird at North
 Carolina State University."

BASE COUNT 162 a 63 c 71 g 141 t

ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 437;
 Best Local Similarity 82.1%; Pred. No. 1.2e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 gggcagaccacgaatccgagatcgacatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 214 GGGCAGCTCCAACTCCGGCTGCGCC 187

RESULT 26
 AJ283475 492 bp mRNA linear EST 30-JUN-2000
 LOCUS AJ283475/c
 DEFINITION 4A3B-AAC-B-03-F Anopheles gambiae immune competent 4A3B Anopheles
 gambiae cDNA clone 4A3B-AAC-B-03, mRNA sequence.
 AJ283475
 AJ283475.1 GI:6931354

KEYWORDS EST.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
REFERENCE 1 (bases 1 to 492)
AUTHORS Dimopoulos, G., Casavant, T. L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M. B. and Kafatos, F. C.
TITLE Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE 20300950
COMMENT Contact: Dimopoulos G
Fotlis C. Kafatos Laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES
source
1. .492
Location/Qualifiers
/organism="Anopheles gambiae"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3B-AAC-B-03"
/clone_lib="Anopheles gambiae immune competent 4A3B"
/cell_line="Immune competent 4A3B"
/lab_host="E. coli DH10B"
/note="Vector: pMT73D-Pac (Pharmacia) with a modified polylinker. Site_1: EcoRI; Site_2: NotI; sequenced from the forward priming site that reads from the 3' end of cDNA. The 4A3B is a directionally cloned and normalized cDNA library that was constructed from the 4A3B cell line oligo-T primed cDNA according to: Bonaldi, Lennon & Soares (1986): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
BASE COUNT 87 a 135 c 157 g 93 t
ORIGIN
Query Match 66.7%; Score 20; DB 9; Length 492;
Best Local Similarity 82.1%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 tgggcagcaccgaagtcggatgcagatc 30
Db 196 GCGCCGACACACGTCGGTTCAGATGC 169
RESULT 27
BG364270/c 530 bp mRNA linear EST 08-MAR-2001
LOCUS dc91g07.y1 NICHHD XGC OOL Xenopus laevis cDNA clone IMAGE:3404724 5
DEFINITION similar to TR:Q9V812 Q9V812 C66550 PROTEIN.; mRNA sequence.
ACCESSION BG364270
VERSION BG364270.1 GI:13253367
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 530)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMI)
DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/ILMI at: info@image.llnl.gov
Seq primer: -40RP from Glibco
High quality sequence stop: 209.
FEATURES
source
1. .530
Location/Qualifiers
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3404724"
/clone_lib="NICHHD XGC OOL"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
BASE COUNT 171 a 113 c 131 g 114 t 1 others
ORIGIN
Query Match 66.7%; Score 20; DB 10; Length 530;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 tgggcagcaccgaagtcggatgcagatc 29
Db 326 TGACGACGCCCATGTGACGATCAGATC 299
RESULT 28
BU096360/c 530 bp mRNA linear EST 12-DEC-2001
LOCUS BU096360 NIBB Mochli normalized Xenopus early gastrula library
DEFINITION Xenopus laevis cDNA clone XL153K16 5', mRNA sequence.
ACCESSION BU096360
VERSION BU096360.1 GI:17597244
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 530)
AUTHORS Kitayama, A., Terasaka, C., Mochli, M., Denu, N., Shin-I, T. and Kohara, Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source
1. .530
Location/Qualifiers
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL153K16"
/clone_lib="NIBB Mochli normalized Xenopus early gastrula library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
BASE COUNT 173 a 118 c 128 g 110 t 1 others
ORIGIN
Query Match 66.7%; Score 20; DB 10; Length 530;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 tgggcagcaccgaagtcggatgcagatc 29
Db 260 TGACGACGCCCATGTGACGATCAGATC 233

```

RESULT 29
AM828856/c 536 bp mRNA linear EST 10-MAY-2001
LOCUS ra69a03.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
DEFINITION CDNA 5' similar to WP:C36E6.B CE20542 ;, mRNA sequence.
ACCESSION AM828856
VERSION AM828856.1 GI:7922655
KEYWORDS EST.
SOURCE southern root-knot nematode.
ORGANISM Meloidogyne incognita
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
AUTHORS Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 536)
McCarte,J., Clifton,S., Chapell,I., B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Rittner,E., Bennett,J., Franklin,C., Tsagaris,I., R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepien
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Uma Rao and David Bird
(david_bird@ensu.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center St.
Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 444.
LOCATION/Qualifiers
FEATURES
source
1..536
/organism="Meloidogyne incognita"
/db_xref="taxon:6306"
/clone_lib="Bird-Rao Meloidogyne incognita J2"
/dev_stage="enriched for 2nd stage juveniles"
/lab_host="XLORL"
/note="Vector: ZAP express - PBKCMV (Stratagene); Site_1:
EcoRI; Site_2: XhoI; Oligo (dT) primed library. CDNA was
constructed and cloned unidirectionally into the vector
within the 5' EcoRI and 3' XhoI sites. This library was
constructed by Dr. Uma Rao and Dr. David Bird at North
Carolina state University."
BASE COUNT 211 a 73 c 91 g 161 t
ORIGIN
Query Match 66.7%; Score 20; DB 9; Length 536;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 gggcagcaccagtcgcatgcagatcc 30
||||| ||||||| ||| |
Db 214 GGGCAGCTCCAGTCCGGCTGCTGCC 187
||||| ||||||| ||| |
RESULT 30
BU038957 547 bp mRNA linear EST 07-DEC-2001
LOCUS BU038957 N1BB Mochii normalized xenopus neurula library xenopus
DEFINITION laevis cDNA clone X1045p19 5', mRNA sequence.
ACCESSION BU038957
VERSION BU038957.1 GI:17408453
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
1 (bases 1 to 547)
Xenopodinae; Xenopus.
Kiyama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasi Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
LOCATION/Qualifiers
FEATURES
source
1..547
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="X1045p19"
/clone_lib="N1BB Mochii normalized xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
BASE COUNT 182 a 118 c 132 g 115 t
ORIGIN
Query Match 66.7%; Score 20; DB 10; Length 547;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 tggcagcaccagtcgcatgcagatc 29
||||| ||| || ||||| |||||
Db 260 TGAGCAGCCCCCATGTACGATCCAGATC 233
||||| ||| || ||||| |||||
RESULT 31
BG710692 563 bp mRNA linear EST 08-MAY-2001
LOCUS BG710692
DEFINITION pglin.pk004.k8 Normalized liver library Gallus gallus cDNA clone
p9lin.pk004.k8 5' similar to p1r1S15904|S15904 alpha-1 proteinase
inhibitor III, variant 1 precursor - rat emb|CA37176.1| (X52984)
alpha(10-inhibitor 3, precursor [Rattus norvegicus]G, mRNA
sequence.
BG710692
VERSION BG710692.1 GI:14004642
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (bases 1 to 563)
Phasianinae; Gallus.
Burnside,J., Morgan,R.W. and Cogburn,L.A.
Chicken ESTs from a normalized liver library
JOURNAL Unpublished (2001)
COMMENT Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu.
LOCATION/Qualifiers
FEATURES
source
1..563
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pglin.pk004.k8"
/clone_lib="Normalized Liver Library"
/sex="Male and Female"
/tissue_type="liver"
/lab_host="E.coli EMDH108"

```

BASE COUNT 117 a /note=Vector: pCMVSPORT 6"
ORIGIN 159 c 184 g 103 t

Query Match 66.7%; Score 20; DB 10; Length 563;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 99gcagcaccagtcgcgatgcagatcc 30
1 ||||| |||| |||| |||| |||| ||
DB 362 GAGCAGACGACGACCCGCTGCAGAGCC 389

RESULT 32
BJ035192/c 572 bp mRNA linear EST 07-DEC-2001
LOCUS BJ035192 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL021e08 5', mRNA sequence.

ACCESSION BJ035192
VERSION BJ035192.1 GI:17414445
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
AUTHORS 1 (bases 1 to 572)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
Source
1..572

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL021e08"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
BASE COUNT 181 a 121 c 146 g 124 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 572;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 1gggcagcaccagtcgcgatgcagatc 29
1 ||||| |||| |||| |||| |||| ||
DB 369 TGAGCAGCCCGCATGTACGATCCAGATC 342

RESULT 33
BJ094267/c 579 bp mRNA linear EST 12-DEC-2001
LOCUS BJ094267 NIBB Mochii normalized Xenopus early gastrula library
DEFINITION Xenopus laevis cDNA clone XL144p09 5', mRNA sequence.

ACCESSION BJ094267
VERSION BJ094267.1 GI:17594218
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 579)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
Source
1..579

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL144p09"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
BASE COUNT 193 a 121 c 145 g 120 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 579;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 1gggcagcaccagtcgcgatgcagatc 29
1 ||||| |||| |||| |||| |||| ||
DB 294 TGAGCAGCCCGCATGTACGATCCAGATC 267

RESULT 34
AV871222/c 653 bp mRNA linear EST 08-NOV-2001
LOCUS AV871222 Nori Satoh unpublished cDNA library, egg Clona
DEFINITION intestinalis cDNA clone r1eg26f08 3', mRNA sequence.

ACCESSION AV871222
VERSION AV871222.1 GI:16858746
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Clona.
AUTHORS 1 (bases 1 to 653)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
TITLE Expressed genes in Clona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
Source
1..653

/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="r1eg26f08"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
BASE COUNT 153 a 140 c 146 g 211 t 3 others
ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 653;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

JOURNAL
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 407.
Location/Qualifiers

FEATURES
source
1..677
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3400926"
/clone_lib="NICHD XGC Emb3"
/tissue_type="embryo (stages 24-25)"
/lab_host="DH10B (phage-resistant)"
/note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

BASE COUNT
217 a 135 c 168 g 157 t

ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 677;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcagatc 29
||| ||||| ||| ||| ||||| |||||
Db 335 TGACGAGCCCATGTACGATCCAGATC 308

RESULT 38
AL593991/c 691 bp mRNA linear EST 30-JUN-2001
LOCUS AL593991 XGC-gastrula Silurana tropicalis cDNA clone Tgas004k14 5',
DEFINITION AL593991 mRNA sequence.
ACCESSION AL593991
VERSION AL593991.1 GI:15006052
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 691)
Huckle, E., Taylor, R., McMurray, A., Ashurst, J. L., Zorn, A. M. and
Rogers, J.
REFERENCE
AUTHORS Sanger Xenopus tropicalis EST project 2001
TITLE Sanger Xenopus tropicalis EST project 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgas004k14.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1..691
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Tgas004k14"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA

was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."

BASE COUNT
229 a 146 c 173 g 143 t

ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 691;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcagatc 29
||| ||||| ||| ||| ||||| |||||
Db 245 TGACGAGCCCATGTACGATCCAGATC 218

RESULT 39
BJ013567 716 bp mRNA linear EST 05-DEC-2001
LOCUS BJ013567 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA190G08 5',
DEFINITION BJ013567 mRNA sequence.
ACCESSION BJ013567
VERSION BJ013567.1 GI:17363442
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 716)
Kohara, Y., Shin-I, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
REFERENCE
AUTHORS Medaka EST Project in Takeda's lab
TITLE Unpublished (2001)
JOURNAL Contact: Tadasu Shin-I
COMMENT Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin1@genes.nig.ac.jp.
Location/Qualifiers
1..716
/organism="Oryzias latipes"
/strain="Hd-R"
/db_xref="taxon:8090"
/clone="MF01SSA190G08"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
BASE COUNT
184 a 193 c 144 g 194 t 1 others

ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 716;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgagtcagatc 28
||||| ||||| ||| ||| |||||
Db 172 CTGGGAGCACACACCTCTCTGTCAGAGT 199

RESULT 40
AL518419 1014 bp mRNA linear EST 13-FEB-2001
LOCUS AL518419 LRT_NF1011.NBC1 Homo sapiens cDNA clone CS0DA009YM24 3
DEFINITION AL518419 LRT_NF1011.NBC1 Homo sapiens cDNA clone CS0DA009YM24 3
ACCESSION AL518419
VERSION AL518419.1 GI:12781912
KEYWORDS EST.

SOURCE	ORGANISM	human.
REFERENCE	Homo sapiens	human.
REFERENCE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 1014)	
REFERENCE	Ll,W.B., Gruber,C., Jesse,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Genoscope	
COMMENT	Genoscope - Centre National de Sequencage	
COMMENT	BP 191 91006 Evry cedex - France	
COMMENT	Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr.	
FEATURES	Location/Qualifiers	
SOURCE	1..1014	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="CS0DA009YM24"	
	/clone_1lb="LTI_NFL011_NBC1"	
	/sex="male"	
	/tissue_type="neuroblastoma cells"	
	/lab_host="DH10B"	
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA	
	was primed with a NotI-Oligo(dT) primer. Five prime end	
	enriched, double-stranded cDNA was digested with Not I and	
	cloned into the Not I and Eco RV sites of the pCMVSPORT 6	
	vector. Library is not normalized, but is the control for	
	the normalized libraries. Library was constructed by life	
	technologies. Contact : Feng Liang Life Technologies, a	
	division of Invitrogen 9800 Medical Center Drive Rockville	
	, Maryland 20850, USA Fax: (1) 301 610 8371 Email :	
	fliang@lifetech.com URL :	
	http://fulllength.invitrogen.com"	
BASE COUNT	169 a 336 c 270 g 231 t 8 others	
ORIGIN		
Query Match	66.7%; Score 20; DB 9; Length 1014;	
Best Local Similarity	82.1%; Pred. No. 1.4e+03;	
Matches	23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY	3 gggcagcaccaatcgcgatcgatcc 30	
Dd	85 GGGCGCCACACAGTCGGAGCAGCATCC 112	
RESULT 41		
CNS03KIE		
LOCUS	CNS03KIE 1040 bp DNA linear GSS 17-MAY-2000	
DEFINITION	Tetradon nigroviridis genome survey sequence. PUC-Orl end of clone	
	033j1l of library G from Tetradon nigroviridis, genomic survey	
	sequence.	
ACCESSION	AL248207.1 GI:7969219	
VERSION	AL248207	
KEYWORDS	GSS: genome survey sequence.	
SOURCE	Tetradon nigroviridis.	
ORGANISM	Tetradon nigroviridis	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	
	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	
	Tetraodontidae; Tetradon.	
REFERENCE	1 (bases 1 to 1040)	
REFERENCE	Roeest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,	
AUTHORS	Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and	
	Weissenbach,J.	
TITLE	Characterization and repeat analysis of the compact genome of the	
	freshwater pufferfish Tetradon nigroviridis	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1040)	
AUTHORS	Roeest-Crollius,H., Jaillon,O., Dasilva,C., Bonneau,L., Fisher,C.,	
	Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,	
	Saurin,W. and Weissenbach,J.	
TITLE	Human gene number estimate provided by genome wide analysis using	
	Tetradon nigroviridis DNA sequence	

/dev-stage="11 weeks old"
/lab-host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 27 a 17 c 28 g 27 t
ORIGIN

Query Match 65.3%; Score 19.6; DB 9; Length 99;
Best Local Similarity 84.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ggcagcaccagtcgcgagtcagatcc 30
||||| ||||| ||||| ||||| |||||
Db 48 GCAGACCAAGTCACATCCAGATCC 23

RESULT 43
BH389734/c
LOCUS BH389734
DEFINITION AG-ND-12512.TR ND-TAM Anopheles gambiae genomic clone AG-ND-12512,
DNA sequence.
ACCESSION BH389734
VERSION BH389734.1 GI:17335875
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae
; Anophelinae.
1 (bases 1 to 499)
Shetty J., Malek J., Koo H., Collins F., Gardner M. and Loftus B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
Other_GSSs: AG-ND-12512.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest
Seq primer: M13 Rev
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..499
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-12512"
/clone_1b="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT 171 a 98 c 77 g 153 t
ORIGIN

Query Match 65.3%; Score 19.6; DB 12; Length 499;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ggcagcaccagtcgcgagtcagatcc 30
||||| || ||||| ||||| ||||| |||||
Db 156 GCAGCAGACACTGCGATGCAGATCC 131

RESULT 44
BM007478/c
LOCUS BM007478
DEFINITION 603616745F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440619 5',
mRNA sequence.
ACCESSION BM007478
VERSION BM007478.1 GI:16521832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 794)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gcgaps-remail.nih.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1913 row: 1 column: 12
High quality sequence start: 7
High quality sequence stop: 397.
Location/Qualifiers

FEATURES
source

1..794
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5440619"
/clone_1b="NIH_MGC_113"
/lab-host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 168 a 209 c 240 g 176 t 1 others
ORIGIN

Query Match 65.3%; Score 19.6; DB 10; Length 794;
Best Local Similarity 84.6%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgagtcagatcc 29
||||| ||||| ||||| ||||| |||||
Db 182 GCCAGCACCAGCCAGATGCAGATCC 157

RESULT 45
CNS037B8
LOCUS CNS037B8
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
001F16 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL231101
VERSION AL231101.1 GI:7890096
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 65.3%; Score 19.6; DB 12; Length 499;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS
1 (bases 1 to 878)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Unpublished
2 (bases 1 to 878)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

Unpublished
3 (bases 1 to 878)
Genoscope.

Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..878
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="001F16"
/clone.lib="G"
/note="Genoscope sequence ID : C0BG001DC08UpI-end : T7"
location/Qualifiers

BASE COUNT
ORIGIN
186 a 242 c 274 g 159 t 17 others

Query Match 65.3%; Score 19.6; DB 12; Length 878;
Best Local Similarity 84.6%; Pred. No.1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcgagatgcag 26
| ||||| ||| ||||| |||
Db 461 CGGGGCGCGCCGCACTCGGATGAG 486

Search completed: September 10, 2002, 01:12:19
Job time: 5851 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 01:47:27 ; Search time 61.65 Seconds
(without alignments)
245.029 Million cell updates/sec

Title: US-09-912-436-6

Perfect score: 719
Sequence: 1 MSPLLRLALLAALLQAPAQ.....EHSQCRCRPPKKDSAVKPD 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747558

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703.5	97.8	206	20	AAW86202
2	649	90.3	188	20	AAW86201
3	644	89.6	188	17	AAW04826
4	644	89.6	188	20	AAW80490
5	644	89.6	206	21	AAV94806
6	644	89.6	207	17	AAW04830
7	644	89.6	207	22	AAW36296
8	644	89.6	221	18	AAW07611
9	644	89.6	221	18	AAV94802
10	641	89.2	207	20	AAW80494
11	636	88.5	221	20	AAW86205

12	634	88.2	188	17	AAW00864	Murine VRF167. Mu
13	634	88.2	207	17	AAW00863	Murine VRF186. Mu
14	630.5	87.7	195	17	AAW04827	Heart vascular end
15	630.5	87.7	195	20	AAW80491	Murine vascular en
16	628	87.3	189	22	AAE09217	Hexa-His-tagged hu
17	624	86.8	167	20	AAW08283	Human growth facto
18	624	86.8	167	21	AAW824082	Human PRO834 matur
19	624	86.8	186	20	AAW08282	Human growth facto
20	618	86.0	795	22	AAV29777	Novel human secret
21	616	85.7	201	17	AAW86236	Human VEGF-3 full
22	612	85.1	133	17	AAW04828	Vascular endotheli
23	612	85.1	133	20	AAW80492	Murine vascular en
24	608.5	84.6	185	20	AAW86235	Human VRF (VEGF-re
25	579	80.5	194	20	AAW86218	Human VEGF-3 trunc
26	571.5	79.5	178	20	AAW86214	Human VRF-2 trunc
27	571	79.4	167	20	AAW86234	Human VEGF-B full
28	549	76.4	160	20	AAW86208	Human VEGF-B trunc
29	548	76.2	189	20	AAW86219	Human VEGF-3 trunc
30	540.5	75.2	173	20	AAW86215	Human VRF-2 trunc
31	529	73.6	101	17	AAW00728	Vascular endotheli
32	527	73.3	155	20	AAW86209	Human VEGF-B trunc
33	520	72.3	184	20	AAW86220	Human VEGF-3 trunc
34	515	71.6	152	20	AAW86210	Human VEGF-B trunc
35	512.5	71.3	168	20	AAW86216	Human VRF-2 trunc
36	504	70.1	150	20	AAW86211	Human VEGF-B trunc
37	494	68.7	179	20	AAW86221	Human VEGF-3 trunc
38	490	68.2	147	20	AAW86212	Human VEGF-B trunc
39	489	68.0	102	17	AAW04824	Vascular endotheli
40	489	68.0	102	20	AAW80488	Murine vascular en
41	486.5	67.7	163	20	AAW86217	Human VRF-2 trunc
42	478	66.5	145	20	AAW86213	Human VEGF-B trunc
43	270.5	37.6	190	20	AAV33440	Paradox virus VEGF
44	269.5	37.5	146	13	AAW22348	Alternative form o
45	269.5	37.5	146	13	AAW27354	Sequence of vascul

ALIGNMENTS

RESULT 1	
ID	AAW86202 standard; protein; 206 AA.
XX	
AC	AAW86202:
XX	
DT	16-FEB-1999 (first entry)
XX	
DE	Human VEGF-related factor (VRF)-2 sequence.
XX	
KW	VEGF, VRF; vascular endothelial growth factor; VEGF-related protein;
KW	recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
KW	coronary; collateral vessel development; cell growth; migration; heart;
KW	lower limb ischemia; stroke; peripheral vascular disease; intestine;
KW	wound healing; skin; VEGF-related factor; VRF; vascular permeability.
XX	
OS	Homo sapiens.
XX	
PN	W09849300-A2.
XX	
PD	05-NOV-1998.
XX	
PF	20-APR-1998; 98WC-US07801.
XX	
PR	25-APR-1997; 97US-0842984.
XX	
PA	(COLL-) COLLATERAL THERAPEUTICS.
XX	
PI	Bohlen P;
XX	
DR	WPI; 1999-009426/01.
XX	
PT	New truncated vascular endothelial growth factor-related protein
PT	subunits - lack part of the N-terminal sequence, used to stimulate

PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Disclosure; Fig 1; 113pp; English.
XX
CC This represents the amino acid sequence of human VRP-2 (a vascular
CC endothelial growth factor (VEGF)-related factor). The invention
CC provides truncated VRP (VEGF-related protein) subunits that have at
CC least one amino acid N-terminal to the first Cys of the core sequence
CC deleted. Host cells transfected or transfected with expression vectors
CC containing nucleic acids encoding the truncated VRP subunits are used to
CC produce the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro,
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability.
XX
SQ Sequence 206 AA:

Query Match 97.8%; Score 703.5; DB 20; Length 206;
Best Local Similarity 99.3%; Pred. No. 4.7e-66;
Matches 135; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSPFLRLTLAALLQAPVOPDAGHQRKVVSWIDYVTRATCQREVVPPLVEL 60
DB 1 mspflrltlllaallqlatqapvsgdpdaphqrkvvswldytracqprevvvplvel 60

QY 61 MGTVAQLVPCVTVQRCGCCPDGLEGVPTGQQLIMIRYPSQLGEMSLSEHS 120
DB 61 mgtvavkqlvpcsvtvqrcgccpdglegvptgqqlimirypsqlgemslsehs 120

QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkdsavkpd 136

RESULT 2
AAW86201
ID AAW86201 standard; protein; 188 AA.
XX
AC AAW86201;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human vascular endothelial growth factor (VEGF)-B sequence.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN WO9849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
FT New truncated vascular endothelial growth factor-related protein

PT subunits - lack part of the N-terminal sequence, used to stimulate
XX angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Disclosure; Fig 1; 113pp; English.
XX
CC This represents the amino acid sequence of human vascular endothelial
CC growth factor (VEGF)-B protein. The invention provides truncated VRP
CC (VEGF-related protein) subunits that have at least one amino acid
CC N-terminal to the first Cys of the core sequence deleted. Host cells
CC transfected or transfected with expression vectors containing nucleic
CC acids encoding the truncated VRP subunits are used to produce the
CC truncated proteins recombinantly. The truncated VRP subunits, optionally
CC expressed from gene therapy vectors, have in vivo and in vitro angiogenic
CC activity and are used to stimulate angiogenesis, particularly coronary
CC collateral vessel development in cases of cardiac ischaemia; to stimulate
CC endothelial cell growth and migration in vitro; to treat heart disease;
CC to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb
CC ischaemia; stroke and peripheral vascular disease); to promote healing of
CC wounds (of skin or intestines), and to increase vascular permeability.
XX
SQ Sequence 188 AA:

Query Match 90.3%; Score 649; DB 20; Length 188;
Best Local Similarity 89.7%; Pred. No. 2.3e-60;
Matches 122; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSPFLRLTLAALLQAPVOPDAGHQRKVVSWIDYVTRATCQREVVPPLVEL 60
DB 1 mspflrltlllaallqlatqapvsgdtpshqkvvswldytracqprevvvplsmel 60

QY 61 MGTVAQLVPCVTVQRCGCCPDGLEGVPTGQQLIMIRYPSQLGEMSLSEHS 120
DB 61 mgtvavkqlvpcsvtvqrcgccpdglegvptgqqlimirypsqlgemslsehs 120

QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkdsavkpd 136

RESULT 3
AAW04826
ID AAW04826 standard; protein; 188 AA.
XX
AC AAW04826;
XX
DT 28-APR-1997 (first entry)
XX
DE Heart vascular endothelial growth factor-B167.
XX
KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
XX
OS Mus musculus.
XX
PN WO9626736-A1.
XX
PD 06-SEP-1996.
XX
PF 01-MAR-1996; 96WO-US02957.
XX
PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
PA (LUDMW-) LUDMWG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX

DR WPI: 1996-412582/41.
DR N-PSDB: AAT37910.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX
PS Claim 18; Page 55-56; 107pp; English.
XX
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences, this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
SQ Sequence 188 AA:

Query Match 89.6%; Score 644; DB 17; Length 188;
Best Local Similarity 89.0%; Pred. No. 7.6e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSPFLRLLLAALQAPAPVSPDAPGHQKRVSMIDVYTRACQPREVVPLTVEL 60
DB 1 mspllrlllvalqlarqtqapvsgfdgpbshqkvvpmldvvaratcqpreevvpismel 60
OY 61 MGTVAQOLVPSCTVQVRCGCCPDGIECVPTGQHOVRMQILMIRPSSQLGEMSLSEHS 120
DB 61 mgnvkvqlvpsectvqcgccpddgilecvptgqhvymqilmlypsqilgmslehs 120
OY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkkesavkpd 136

RESULT 4
AAW80490
ID AAW80490 standard; Protein: 188 AA.
XX
XX AAW80490;
AC
XX
DT 29-JAN-1999 (first entry)
XX
DE Murine vascular endothelial growth factor (VEGF)-B167.
XX
XX Vascular endothelial growth factor; VEGF: proliferation; mouse;
XX
XX Vascular endothelial cell; angiogenesis; tissue growth; organ repair.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 1 /note="encoded by G"
XX
XX FT
XX
XX PN US5840693-A.
XX
XX PD 24-NOV-1998.

XX
XX 01-MAR-1996; 96US-0609443.
XX
XX 01-MAR-1996; 96US-0609443.
XX
XX 01-MAR-1995; 95US-0397651.
XX
XX 06-JUN-1995; 95US-0469427.
XX
XX 06-DEC-1995; 95US-0569063.
XX
XX (LUDM-) LUDMIG INST CANCER RES.
XX
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX
XX WPI: 1999-034079/03.
XX
XX N-PSDB: AAV63564.
XX
XX
XX Vascular endothelial growth factor-B isoforms, and DNA encoding
XX them - useful for inducing angiogenesis and cellular proliferation,
XX and raising antibodies to inhibit activities in e.g. tumours
XX
XX Claim 1; Fig 4; 52pp; English.
XX
XX
XX The present sequence represents murine vascular endothelial growth factor
XX (VEGF)-B167. VEGF proteins are used for promoting proliferation of
XX endothelial cells and for stimulating angiogenesis (the proliferation
XX of new capillaries form pre-existing blood vessels). These activities
XX are useful for treating tissue growth and repair, including organ
XX repair. This is also useful in pregnancy, in follicle development,
XX as these processes must occur in development of the placenta. The
XX proteins can also be used to raise antibodies, either for use in
XX detection of the proteins or as inhibitors of their action. This is
XX especially useful as angiogenesis is required by tumours as they need
XX new blood supplies to grow and proliferate.
XX
SQ Sequence 188 AA:

Query Match 89.6%; Score 644; DB 20; Length 188;
Best Local Similarity 89.0%; Pred. No. 7.6e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSPFLRLLLAALQAPAPVSPDAPGHQKRVSMIDVYTRACQPREVVPLTVEL 60
DB 1 mspllrlllvalqlarqtqapvsgfdgpbshqkvvpmldvvaratcqpreevvpismel 60
OY 61 MGTVAQOLVPSCTVQVRCGCCPDGIECVPTGQHOVRMQILMIRPSSQLGEMSLSEHS 120
DB 61 mgnvkvqlvpsectvqcgccpddgilecvptgqhvymqilmlypsqilgmslehs 120
OY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkkesavkpd 136

RESULT 5
AA94806
ID AA94806 standard; Protein: 206 AA.
XX
XX AA94806;
AC
XX
DT 19-JUN-2000 (first entry)
XX
XX Human VEGF-3 splice variant.
XX
XX Vascular endothelial growth factor 3; VEGF-3; splice variant;
XX
XX Vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
XX
XX cancer; wounds; autoimmune disease; HIV; inflammation; heart disease.
XX
XX Homo sapiens.
XX
XX WO200009148-A1.
XX
XX PD 24-FEB-2000.

```
XX 10-AUG-1999; 99WO-US18054.
PF 10-AUG-1999; 98US-0132088.
PR 10-FEB-1999; 99US-0244694.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Hu J, Olsen HS, Rosen CA;
PI WPI: 2000-224173/19.
DR
XX
XX New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -
XX
XX Claim 25; Fig 4; 209pp; English.
PS
XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. The present sequence represents a splice
CC variant of human VEGF-3.
XX
SQ Sequence 206 AA;

Query Match 89.6%; Score 644; DB 21; Length 206;
Best Local Similarity 100.0%; Pred. NO. 8.4e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PAQAFVSQPDAPGHQKRVSMIDVYTRATCOPREVVVPLTVELMGTVAKOLPSCVTYQR 77
Db 17 paeqavspdpdephqgrkxvswldytracqprevvvplvelmgtkqlvpscvtvgr 76
QY 78 CGGCCPDGDLCEVPTGQHQRVMQILMIRYSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 77 cggccpddgdlcevpptgqhqrvmqilmirypsqsqlemsehsqecrpkkkdsavkpd 135

RESULT 6
AAW04830
ID AAW04830 standard; Protein; 207 AA.
XX
XX AAW04830;
AC
XX
XX 28-APR-1997 (first entry)
DT
XX
XX Vascular endothelial growth factor-B186.
DE
XX
XX Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
XX
XX Mus musculus.
OS
XX
XX W09626736-A1.
PN
XX
```

```
PD 06-SEP-1996.
XX
XX 01-MAR-1996; 96WO-US02957.
PF
XX
XX 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
XX 06-JUN-1995; 95US-0469427.
XX
XX (LUDWIG) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alltalo K, Eriksson U, Olofsson B, Rajusola K;
PI WPI: 1996-412582/41.
XX
XX N-PSDB; AAT37914.
DR
XX
XX Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX Claim 18; Page 60-61; 107pp; English.
PS
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences; this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
XX Sequence 207 AA;

Query Match 89.6%; Score 644; DB 17; Length 207;
Best Local Similarity 89.0%; Pred. NO. 8.5e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPILRRLLLAALQADPAQAPVSPDAPGHQKRVSMIDVYTRATCOPREVVVPLVEL 60
Db 1 mspilrrlllvaillqartcpqsfqgshqkxvswldytracqprevvvplsmel 60
QY 61 MGTVAKQLVPSCVTVQRCGGCCPDGDLCEVPTGQHQRVMQILMIRYSSQLGEMSLSEHS 120
Db 61 mgnvkvkqlvpscvtvqrcggccpddgdlcevpptgqhqrvmqilmirypsqsqlemsehs 120
QY 121 QCECRPKKDSAVKPD 136
Db 121 qcecrpkkkdsavkpd 136

RESULT 7
AAB36296
ID AAB36296 standard; Protein; 207 AA.
XX
XX AAB36296;
AC
XX
XX 23-FEB-2001 (first entry)
DT
XX
XX Human vascular endothelial growth factor VEGF-B186.
DE
```

XX Human: vascular endothelial growth factor: VEGF-B; bone growth;
 KM angiogenesis; neovascularisation; bone break; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200064261-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-US11096.
 XX
 PR 26-APR-1999; 99US-0130935.
 XX
 PA (LUDWIG) LUDWIG INST CANCER RES.
 XX (UTHE-) UNIV HELSINKI LICENSING LTD.
 PI Aase K, Kaipainen A, Olofsson B, Aitalo K, Eriksson U;
 XX
 DR WPI: 2001-015797/02.
 DR N-PSDB; AAC81776.
 XX
 PT Use of a polypeptide having the biological activity of vascular
 PT endothelial growth factor-B for stimulating angiogenesis of bone,
 PT healing of bone fractures and enhancing acceptance of an implant to
 PT bone -
 PS Claim 1; Page 37-38; 43pp; English.
 XX
 CC The present invention discloses a use for human vascular endothelial
 CC growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This
 CC can be used to promote bone growth, stimulate the healing of breaks or
 CC fractures, secure an implant to the bone and to alleviate inflammation in
 CC long bones.
 XX
 SQ Sequence 207 AA;

Query Match 89.6%; Score 644; DB 22; Length 207;
 Best Local Similarity 89.0%; Pred. No. 8.5e-60;
 Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPLLRLRLAALQLAPAPVSPDPAGHQRKVSIMIDYTRATCOPREVVPPLVEL 60
 Db 1 mspllrrlllvaallqlartqavsfqfgrshqkvvpwidyaratcprevvvplsmel 60

QY 61 MGTVAKQLVPSCVTVQRGCGCPDDGLECVPTGQHOVRMQLIMIRYPSQLGEMSLREHS 120
 Db 61 mgtvakkqlvpscvtvqrqcgccpddglecvptgqhvymqllimrypsqliemslrehs 120

QY 121 QCECRPKKDSAVKPD 136
 Db 121 qcecrpkkesavkpd 136

RESULT 8
 AAM07611
 ID AAM07611 standard; Protein; 221 AA.
 XX
 AC AAM07611;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human vascular endothelial growth factor 3.
 XX
 KW Human vascular endothelial growth factor; hVEGF3; angiogenesis;
 KW tumour; inflammation; rheumatoid arthritis; diabetic retinopathy;
 KW psoriasis; bone; periodontium; ligament; antagonist.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region 69..82 Location/Qualifiers

FT /label= PDGF/VEGF_family_signature
 FT /note= "conserved PXCXXXXXCGCCN motif"
 XX
 PN WO9639421-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1995; 95WO-US07283.
 XX
 PR 06-JUN-1995; 95WO-US07283.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen H, Rosen CA, Hu JS;
 XX
 DR WPI: 1997-043056/04.
 DR N-PSDB; AAT44071.
 XX
 PT DNA encoding human vascular endothelial growth factor 3 - useful to
 PT develop prods. for, e.g. stimulating angiogenesis or treating
 PT tumours, inflammation or rheumatoid arthritis
 PS Claim 11; Page 44; 56pp; English.
 XX
 CC This sequence is that of human vascular endothelial growth factor 3
 CC (VEGF3). The growth factor can be used to stimulate angiogenesis and
 CC wound healing, and to promote vascular tissue repair. It can also be
 CC used to induce the growth of damaged bone, periodontium or ligament
 CC tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
 CC treat diabetic retinopathy, inflammation, rheumatoid arthritis or
 CC psoriasis. VEGF3 is structurally related to the PDGF/VEGF family
 CC and it includes the conserved signature motif for the family (see
 CC features table).
 XX
 SQ Sequence 221 AA;

Query Match 89.6%; Score 644; DB 18; Length 221;
 Best Local Similarity 100.0%; Pred. No. 9.2e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PAQAPVSPDPAGHQRKVSIMIDYTRATCOPREVVPPLVELMGTVAKQLVPSCVTVQR 77
 Db 17 paqapvsgpdapgygrkvvswidvtracqprevvvplvelmgvtaqqlvpscvtvqr 76

QY 78 CGGCCPDDGLECVPTGQHOVRMQLIMIRYPSQLGEMSLREHSQCCECRPKKDSAVKPD 136
 Db 77 cggccpddglecvptgqhvymqllimrypsqliemslrehsqcecrpkksavkpd 135

RESULT 9
 AAY94802
 ID AAY94802 standard; Protein; 221 AA.
 XX
 AC AAY94802;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human VEGF-3.
 XX
 KW Vascular endothelial growth factor 3; VEGF-3; vascular expression;
 KW lymphatic; bone marrow; colon; heart; kidney; ovary; cancer; wounds;
 KW autoimmune disease; HIV; inflammation; heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200009148-A1.
 XX
 PD 24-FEB-2000.
 XX
 PF 10-AUG-1999; 99WO-US18054.
 XX
 PR 10-AUG-1998; 98US-0132088.

PR 10-FEB-1999; 99US-0244694.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Hu J, Olsen HS, Rosen CA;
 XX
 DR WPI; 2000-224173/19.
 XX

PT New human gene encoding vascular endothelial growth factor 3 and
 PT polypeptide encoded by the gene is useful for treating various
 PT disorders associated with vascular and lymphatic system -
 XX

PS Claim 11; Fig 1; 209pp; English.

XX
 CC The invention relates to human vascular endothelial growth factor 3
 CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
 CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding
 CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
 CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
 CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
 CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
 CC being consistent with vascular and lymphatic specific expression. VEGF-3
 CC proteins and nucleotides are useful in preventing, treating or
 CC ameliorating various disorders and conditions associated with the
 CC vascular and lymphatic systems. These conditions and disorders include
 CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
 CC disease. VEGF-3 may also be used to identify its own binding partners.
 CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
 CC an alternative to restriction fragment length polymorphism (RFLP). The
 CC nucleotides are also useful to prepare PCR primers for amplifying an
 CC isolating selected DNAs. The present sequence represents human VEGF-3.
 CC
 XX
 SQ Sequence 221 AA;

Query Match 89.6%; Score 644; DB 21; Length 221;
 Best Local Similarity 100.0%; Pred. No. 9.2e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PAQAPVSDPAPGHRKRVSMIDVYTRATCQPREVVPLTVELMGVYAKOLVPSCTVYOR 77
 DB 17 padapvsgpdapghqkvsvsldvyltralcqprevvpltlvelmgvayakqlvpscvlvrq 76
 OY 78 CGGCCPDGDLCEVPTGSOHOVRMOILMIRYPSOLGEMSLSEHSQCCRPKKKDSAVKPD 136
 DB 77 cgccpddgdlcevptgsohovrmolmiryssolgemslsehsqccrpkksavkpd 135

RESULT 10

AAW80494
 ID AAW80494 standard; Protein; 207 AA.

AC AAW80494;

DT 29-JAN-1999 (first entry)

DE Murine vascular endothelial growth factor (VEGF)-B186.

KM Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KM endothelial cell; angiogenesis; tissue growth; organ repair.

OS Mus sp.

XX US5840693-A.

PN 24-NOV-1998.

PD 01-MAR-1996; 96US-0609443.

XX 01-MAR-1996; 96US-0609443.

PR 01-MAR-1996; 96US-0609443.

PR 06-JUN-1995; 95US-0397651.

PR 06-DEC-1995; 95US-0469427.

PR 06-DEC-1995; 95US-0569063.

XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
 XX
 DR WPI; 1999-034079/03.
 XX
 DR N-PDB; AAV63568.

PT Vascular endothelial growth factor-B isoforms, and DNA encoding
 PT them - useful for inducing angiogenesis and cellular proliferation,
 PT and raising antibodies to inhibit activities in e.g. tumours
 XX

PS Claim 1; Fig 13; 52pp; English.

XX
 CC The present sequence represents murine vascular endothelial growth factor
 CC (VEGF)-B186. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries form pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.
 CC
 XX

SQ Sequence 207 AA;

Query Match 89.2%; Score 641; DB 20; Length 207;
 Best Local Similarity 88.2%; Pred. No. 1.8e-59;
 Matches 120; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSPLRLRLIALMLQAPAPVSDPAPGHRKRVSMIDVYTRATCQPREVVPLTVEL 60
 DB 1 msplrlrlilvallqlatqapvqdgpsbqkvvpwldvyltralcqprevvplsmel 60
 OY 61 MGVYAKOLVPSCTVYORCGGCCPDGDLCEVPTGSOHOVRMOILMIRYPSOLGEMSLSEHS 120
 DB 61 mgnvkvqilvpsctvyrqcgccpddgdlcevptgsohovrmolmiryssolgemslsehs 120

OY 121 QCECRPKKRDASAVKPD 136
 DB 121 qcecrpkksavkpd 136

RESULT 11

AAW86205
 ID AAW86205 standard; protein; 221 AA.

AC AAW86205;

DT 16-FEB-1999 (first entry)

DE Human vascular endothelial growth factor (VEGF)-3 sequence.

KM VEGF: VBP: vascular endothelial growth factor; VEGF-related protein;
 KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KM coronary; collateral vessel development; cell growth; migration; heart;
 KM lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KM wound healing; skin; vascular permeability.

XX Homo sapiens.

PN WO9849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

XX Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
XX
DR WPI; 1996-412774/41.
DR N-PSDB; AAT13809.
XX
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
XX
PS Example 5; Fig 9; 113pp; English.
XX
CC VRF186 (AAW00863) is the murine homologue of human vascular endothelial
CC growth factor-like polypeptide SOM175 (AAW00725), a protein capable of
CC inducing astroglial proliferation and of promoting neural survival
CC and/or proliferation. Its amino acid sequence was deduced from a
CC cDNA clone (AAT13809) isolated from a new-born mouse brain cDNA
CC library. An alternatively spliced variant, VRF169 (AAW00864), was
CC also identified.
XX
SQ Sequence 207 AA:

Query Match 88.2%; Score 634; DB 17; Length 207;
Best Local Similarity 87.5%; Pred. No. 9.5e-59;
Matches 119; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSPFLRLRLIAALLOAPAPYSDPAPGHOKRVSMIDVYRANCOPEVVVPLTVEL 60
Db 1 MSPFLRLRLIAALLOAPAPYSDPAPGHOKRVSMIDVYRANCOPEVVVPLTVEL 60
QY 61 MGTVAKQLVPSCTVVRGCGCCPDGLEGVPTGQHQRMOILMIRYPSQLGEMSLSEHS 120
Db 61 MGNVNVKQLVPSCTVGRGCGCCPDGLEGVPTGQHQRMOILMIRYPSQLGEMSLSEHS 120
QY 121 QCECRPKKDSAVKPD 136
Db 121 QCECRPKKDSAVKPD 136
QY 121 QCECRPKKDSAVKPD 136
Db 121 QCECRPKKDSAVKPD 136

RESULT 14
AAW04827
ID AAW04827 standard; Protein; 195 AA.
AC AAW04827;
XX
DT 28-APR-1997 (first entry)
XX
DE Heart vascular endothelial growth factor-B174.
XX
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
XX
OS Mus musculus.
XX
PN W09626736-A1.
XX
PD 06-SEP-1996.
XX
PF 01-MAR-1996; 96WO-US02957.
XX
PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
PA (LUDWIG-) LUDWIG INST CANCER RES.
PA (UYHE-) UNITV HELSINKI LICENSING LTD OY.
XX
PI Aitalo K, Eriksson U, Olofsson B, Pajusola K;

XX
DR WPI; 1996-412582/41.
DR N-PSDB; AAT37911.
XX
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
PS Claim 18; Page 56-57; 107pp; English.
XX
CC AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences, this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
SQ Sequence. 195 AA:

Query Match 87.7%; Score 630.5; DB 17; Length 195;
Best Local Similarity 84.6%; Pred. No. 2.1e-58;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 MSPFLRLRLIAALLOAPAPYSDPAPGHOKRVSMIDVYRANCOPEVVVPLTVEL 60
Db 1 MSPFLRLRLIAALLOAPAPYSDPAPGHOKRVSMIDVYRANCOPEVVVPLTVEL 60
QY 61 MGTVAKQLVPSCTVVRGCGCCPDGLEGVPTGQHQRMOILMIRYPSQLGEMSLSEHS 113
Db 61 MGNVNVKQLVPSCTVGRGCGCCPDGLEGVPTGQHQRMOILMIRYPSQLGEMSLSEHS 120
QY 114 MSLEHSHQCECRPKKDSAVKPD 136
Db 121 MSLEHSHQCECRPKKDSAVKPD 143

RESULT 15
AAW80491
ID AAW80491 standard; Protein; 195 AA.
AC AAW80491;
XX
DT 29-JAN-1999 (first entry)
XX
DE Murine vascular endothelial growth factor (VEGF)-B174.
XX
KW Vascular endothelial growth factor; VEGF; proliferation; mouse;
KW endothelial cell; angiogenesis; tissue growth; organ repair.
XX
OS Mus sp.
XX
PN US5840693-A.
XX
PD 24-NOV-1998.
XX
PF 01-MAR-1996; 96US-0609443.
XX

PR 01-MAR-1996: 96US-0609443.
PR 01-MAR-1995: 95US-0397651.
PR 06-JUN-1995: 95US-0469427.
PR 06-DEC-1995: 95US-0569063.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
XX
XX WPI: 1999-034079/03.
DR N-PSDB: AAV63565.
XX
XX Vascular endothelial growth factor-B isoforms, and DNA encoding
PT them - useful for inducing angiogenesis and cellular proliferation,
PT and raising antibodies to inhibit activities in e.g. tumours
XX
XX Claim 1: Fig 6; 52pp; English.
XX
XX The present sequence represents murine vascular endothelial growth factor
CC (VEGF)-B174. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
CC new blood supplies to grow and proliferate.
XX
SQ Sequence 195 AA;

Query Match 87.7%; Score 630.5; DB 20; Length 195;
Best Local Similarity 84.6%; Pred. No. 2.1e-58;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

OY 1 MSPLIRLLMALLOLAQAQVSGPDAPGHQRKRVSMIDVYTRATCQPREVVPVLTVEL 60
Db 1 msplirlllvalqlartqavsgfdgpsnqkxvwpwdyvaratcqprrvvpvlsmel 60
OY 61 MGTVAKOLVPSCVTVQRCGCCPDGDLCEVPTGQHQRN-----QIMIRYPSQSGE 113
Db 61 mgnvvtqglvpscvtvqrcgscppddgilecvptgqhqrvmqvpqmgqilmtypsqsglge 120
OY 114 MSLEHSGCECRPKKKDSAVKPD 136
Db 121 mslehsqcecrpkkkksavkpd 143

RESULT 16
AAE09217
ID AAE09217 standard; Protein: 189 AA.
XX
XX AAE09217;
XX
DT 19-NOV-2001 (first entry)
XX
XX Hexa-His-tagged human VEGF-B167 protein.
XX
XX Protein purification: affinity chromatography; angiogenesis;
KW vascular endothelial growth factor; autotransplantation; tumour;
KW rheumatoid arthritis; diabetic retinopathy; His tag; human; VEGF-B167.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
FH Peptide 1..21
FT Region /label- leader_sequence
FT 5..10
FT /label- Hexa-His-tag
FT Cleavage-site 14..19

FT /label= Thrombin_cleavage_site
FT Protein 22..189
FT /note= "Mature human VEGF-B167"
XX
XX WO200160861-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-AU00160.
XX
XX 16-FEB-2000; 2000AU-0005681.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Scrofani SDB, Nash AD, Fabri LJ, Mackenzie AW, Scotney PD;
PI
XX
XX WPI: 2001-541645/60.
DR N-PSDB: AAD16128.
XX
XX
XX Purifying a protein or polypeptide, e.g. vascular endothelial growth
PT factor (VEGF)-B isoform, comprises subjecting a biological sample to
PT affinity chromatography to allow the full length to bind and not the
PT truncated or clipped forms -
XX
XX Example 1: Fig 1; 77pp; English.
XX
XX The invention relates to a method for purifying a polypeptide comprising
CC subjecting a biological sample to chromatography with an affinity matrix
CC for an N- or C-terminal region of the polypeptide, that permits binding
CC of full length molecule and not the truncated form. The method is useful
CC for purifying human vascular endothelial growth factor (VEGF) especially
CC VEGF-B isoforms e.g. VEGF-B167, VEGF-B186 and VEGF-B10-108. VEGF is
CC involved in normal angiogenesis including formation of the corpus luteum,
CC placental development, regulation of vascular permeability, inflammatory
CC angiogenesis, autotransplantation and human diseases such as tumour
CC promoting angiogenesis, rheumatoid arthritis and diabetes related
CC retinopathy. The VEGF molecules are useful in therapeutic protocols and
CC diagnostic assays. The present sequence is hexa-histidine-tagged human
CC VEGF-B167 protein.
XX
SQ Sequence 189 AA;

Query Match 87.3%; Score 628; DB 22; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 APVSQPDAPGHQRKRVSMIDVYTRATCQPREVVPVLTVELMGTVAKOLVPSCVTVQRCG 80
Db 22 apvsqpdapghqrkvswldvtrctcqprrvvpvlvelmgvtakqlvpscvtvqrcg 81
OY 81 CCPDGLCEVPTGQHQRNQMILMIRYPSQSGEMLSEHSGCECRPKKKDSAVKPD 136
Db 82 ccpddgilecvptgqhqrvmqilmitypsqsgelmslehsqcecrpkkkdsavkpd 137

RESULT 17
AAV08283
ID AAV08283 standard; Protein: 167 AA.
XX
XX AAV08283;
XX
DT 14-JUL-1999 (first entry)
XX
XX Human growth factor protein fragment VEGF-B167.
XX
XX Growth factor: human; dimer; cysteine knot; cellular inclusion body;
KW pharmaceutical.
XX
XX Homo sapiens.
OS
XX
XX DE19748734-A1.
XX
XX

PD 06-MAY-1999.
XX
PR 05-NOV-1997; 97DE-1048734.
XX
PR 05-NOV-1997; 97DE-1048734.
XX
XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PI Erdmann H, Kaerst U, Mueller C, Rinas U, Welch H;
DR WPI; 1999-278785/24.
XX
XX
PT Preparing active growth factor dimers from inclusion bodies in high
PS yield
XX
PS Claim 14; Page 8; 14pp; German.
XX
CC This invention describes the novel preparation of biologically active
CC dimers of recombinant human growth factors of the cysteine knot family
CC starting from cellular inclusion bodies. Such dimers are are useful in
CC pharmaceutical compositions and the method provides yields of 31-39.7%,
CC in examples, compared with about 10% for the conventional method (see
CC Biochemistry, 28 (1989) 2956). AAY08228-Y08301 are human growth factor
CC protein fragments used in the method of the invention.
XX
XX Sequence 167 AA;
SQ
Query Match 86.8%; Score 624; DB 20; Length 167;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 PVSOPDAPGHQRKVVNSIDVYTRATCPREVVPVLVTELMGTAKOLVPSCVTVQRCGCG 81
DB 1 pvsqpdapghqrkvvnsidvyratcqprevvplvtevmgtavakqlvpscvtrqrcgyc 60
QY 82 CPDDGLECVPTGQHOVMQILMIRYSSQSGEMSLSHSCCECRPKKDSAVKPD 136
DB 61 cpddglecvptgqhvmqilmitrypsqsgleehsqcecrpkkkdsavkpd 115
RESULT 18
AAB24082 standard; Protein; 167 AA.
XX
AC AAB24082;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO834 mature VEGF-b protein sequence SEQ ID NO:69.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; angiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypochalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PE 06-JAN-2000; 2000WO-US00376.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.

PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
DR WPI; 2000-572270/53.
XX
XX N-PSDB; AAC58391.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
PS Claim 61; Fig 50; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, valve, thyroid, hepatic
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoelec disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
XX Sequence 167 AA;
SQ
Query Match 86.8%; Score 624; DB 21; Length 167;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 PVSOPDAPGHQRKVVNSIDVYTRATCPREVVPVLVTELMGTAKOLVPSCVTVQRCGCG 81
DB 1 pvsqpdapghqrkvvnsidvyratcqprevvplvtevmgtavakqlvpscvtrqrcgyc 60
QY 82 CPDDGLECVPTGQHOVMQILMIRYSSQSGEMSLSHSCCECRPKKDSAVKPD 136
DB 61 cpddglecvptgqhvmqilmitrypsqsgleehsqcecrpkkkdsavkpd 115
RESULT 19
AAY08282 standard; Protein; 186 AA.
XX
AC AAY08282;
XX
DT 14-JUL-1999 (first entry)
XX
DE Human growth factor protein fragment VEGF-B186.
XX
KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
KW pharmaceutical.
XX
OS Homo sapiens.
XX
PN DE19748734-A1.

XX 06-MAY-1999.
 PD
 XX 05-NOV-1997; 97DE-1048734.
 PF
 XX 05-NOV-1997; 97DE-1048734.
 PR
 XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PA
 XX Erdmann H, Kaerst U, Mueller C, Rinas U, Welch H;
 PI
 XX WPI; 1999-278785/24.
 DR
 XX
 PT Preparing active growth factor dimers from inclusion bodies in high
 PT yield
 PS
 XX Claim 14; Page 8; 14pp; German.
 CC This invention describes the novel preparation of biologically active
 CC dimers of recombinant human growth factors of the cysteine knot family
 CC starting from cellular inclusion bodies. Such dimers are are useful in
 CC pharmaceutical compositions and the method provides yields of 31-39.7%,
 CC in examples, compared with about 10% for the conventional method (see
 CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
 CC protein fragments used in the method of the invention.
 CC
 XX
 SQ Sequence 186 AA;

Query Match 86.8%; Score 624; DB 20; Length 186;
 Best Local Similarity 100.0%; Pred. No. 9.5e-58;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 PVSQPDAGHQKRVSWIDYTRATCPREVVPPLTVELMGTVAKOLVPSCVTVORCGC 81
 Db 1 pvsqpdagbhqrvswidyltracqprevvpltlvclmgtvakqlvpscvtlvqrcgc 60
 OY 82 CPDDLECVPTGOHQRVMOILMIRPSSQLGEMSLSEHSQCCRCRKKDSAYKPD 136
 Db 61 cpddglecvptgohqrvmoilmlirpssqlgemslsehsqccrcrpkksavkpd 115

RESULT 20
 AAU29777
 ID AAU29777 standard; Protein: 795 AA.
 AC AAU29777;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #268.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PS
 XX Claim 20; Page 193; 765pp; English.
 PS
 XX

The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 CC
 XX
 SQ Sequence 795 AA;

Query Match 86.0%; Score 618; DB 22; Length 795;
 Best Local Similarity 86.7%; Pred. No. 2.3e-56;
 Matches 117; Conservative 2; Mismatches 4; Indels 12; Gaps 1;

OY 14 LQLAQAQAVSQPDAGHQKRVSWIDYTRATCPREVVPPLTVELMGTVAKOLVPSCV 73
 Db 446 lqltqapvsqpdagbhqrvswidyltracqprevvpltlvclmgtvakqlvpscv 505
 OY 74 TVQRGCGCCPDGELCVPTGOHQRV-----MQLMIRPSSQLGEMSLSEHSQ 121
 Db 506 tvqrcgscppddglecvptgohqrvmlgtwngngmqilmlyrpsqlgemslsehsq 565
 OY 122 CECRPRKKRDSAYKPD 136
 Db 566 cecrprkkdsavkpd 580

RESULT 21
 AAW86236
 ID AAW86236 standard; Protein: 201 AA.
 AC AAW86236;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-3 full length sequence.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PI Bohlen P;
 XX

DR WPI: 1999-009426/01.
 XX
 PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS Claim 5; Fig 2C; 113pp; English.
 XX
 CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP
 CC sequences from which the truncated fragments are created.
 CC
 SQ Sequence 201 AA;
 Query Match 85.7%; Score 616; DB 20; Length 201;
 Best Local Similarity 99.1%; Pred. No. 7.2e-57;
 Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 22 PVSQPDAPGHRKVVSMIDVYTRATCOPREVVPPLVLMGTAVAKOLVSCVTVOQCGGC 81
 DB 1 PVSQPDAPGHRKVVSMIDVYTRATCOPREVVPPLVLMGTAVAKOLVSCVTVOQCGGC 60
 QY 82 CPDDGELCVPTGQHQVBMQILMIRYPSQSGEMLEESHOCECPKPKKDSAVKPD 136
 DB 61 CPDDGELCVPTGQHQVBMQILMIRYPSQSGEMLEESHOCECPKPKKDSAVKPD 115
 RESULT 22
 AAW04828 standard; Protein: 133 AA.
 AC AAW04828;
 DT 28-APR-1997 (first entry)
 DE Vascular endothelial growth factor-B112.
 KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Mus musculus.
 PN W09626736-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996; 96MO-US02957.
 PR 06-DEC-1995; 95US-0569063.
 PR 01-MAR-1995; 95US-0397651.
 PR 06-JUN-1995; 95US-0469427.
 PA (LUDM-) LUDMIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
 XX

DR WPI: 1996-412582/41.
 DR N-PSDB: AAT37912.
 XX
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 XX
 PS Claim 18; Page 58; 107pp; English.
 XX
 CC AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which
 CC it is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting
 CC endothelial cell growth during normal embryonic development, wound
 CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
 CC the invention share the angiogenic and other properties of VEGF, but are
 CC distributed and expressed in tissues differently to VEGF. The proteins
 CC can therefore be used to accelerate angiogenesis in wound healing.
 CC Antibodies against the proteins can be used for inhibiting angiogenesis.
 CC The antibodies can also be used diagnostically to quantitatively detect
 CC VEGF-B. Primers complementary to the coding sequences for the proteins
 CC of the invention can also be used to detect VEGF-B coding sequences.
 CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
 CC indicator of metastatic risk. VEGF-B expression in a cell can be
 CC regarded using antisense sequences direct against the VEGF coding
 CC sequences, this is especially useful in retarding VEGF expression in
 CC tumour cells.
 CC
 SQ Sequence 133 AA;
 Query Match 85.1%; Score 612; DB 17; Length 133;
 Best Local Similarity 89.1%; Pred. No. 1.2e-56;
 Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MSPLRLRLAALQLAPACAPVSQDPAPGHRKVVSMIDVYTRATCOPREVVPPLVVEL 60
 DB 1 MSPLRLRLAALQLAPACAPVSQDPAPGHRKVVSMIDVYTRATCOPREVVPPLVVEL 60
 QY 61 MGTAVAKOLVSCVTVOQCGGCPCDDGLBCVPTGQHQVBMQILMIRYPSQSGEMLEES 120
 DB 61 MGNVVKQLVPSCVTVGCGCCPDDGLBCVPTGQHQVBMQILMIRYPSQSGEMLEES 120
 QY 121 QCCECRPKKK 129
 DB 121 QCCECRPKKK 129
 RESULT 23
 AAW80492 standard; Protein: 133 AA.
 ID AAW80492
 AC AAW80492;
 DT 29-JAN-1999 (first entry)
 DE Murine vascular endothelial growth factor (VEGF)-B112.
 KW Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KW endothelial cell; angiogenesis; tissue growth; organ repair.
 OS Mus sp.
 PN US5840693-A.
 PD 24-NOV-1998.
 PF 01-MAR-1996; 96US-0609443.
 PR 01-MAR-1996; 96US-0609443.
 XX

PR 01-MAR-1995; 95US-0397651.
 PR 06-JUN-1995; 95US-0469427.
 PR 06-DEC-1995; 95US-0569063.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Aittalo K, Eriksson U, Olofsson B, Pajusola K;
 XX
 XX WPI: 1999-034079/03.
 DR N-PSDB: AAV63566.
 XX
 XX Vascular endothelial growth factor-B iso:forms, and DNA encoding
 PT them - useful for inducing angiogenesis and cellular proliferation,
 PT and raising antibodies to inhibit activities in e.g. tumours
 XX
 XX Claim 1; Fig 8; 52pp; English.
 XX
 CC The present sequence represents murine vascular endothelial growth factor
 CC (VEGF)-B112. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries from pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.
 CC
 XX Sequence 133 AA;
 SQ

Query Match 85.1%; Score 612; DB 20; Length 133;
 Best Local Similarity 89.1%; Pred. No. 1.2e-56;
 Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MSPLLRLLLAALLQAPAPVSGPDAPGHORRVSMIDVYTRATCQPREVYVPLVTEL 60
 Db 1 mspllrlllvallqlartqpsqfddgshqkvvpwldvyaratcqprrvvpplsmel 60
 QY 61 MGTAKQLVPSCVTVVORCGCCPDGDLGECVPTGQHVMQILMIRYSSSOLGEMSLSEHS 120
 Db 61 mgtavkqlvpscvtrvqrgcgcpddgdlgcvptgqhvrmqilmlrlypsqjgmslehs 120
 QY 121 QCECRPKKK 129
 Db 121 qcecrpkkk 129

RESULT 24
 AAW86235
 ID AAW86235 standard; protein; 185 AA.
 XX
 AC AAW86235;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VRF (VEGF-related factor)-2 full length sequence.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability; VRF.
 XX
 OS Homo sapiens.
 XX
 PN W09849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX

XX
 PR 25-APR-1997; 97US-0842964.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PI Bohlen P;
 XX
 DR WPI: 1999-009426/01.
 XX
 XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS Claim 5; Fig 2B; 113pp; English.
 XX
 CC The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86234 to AAW86239 represent full length VRF
 CC sequences from which the truncated fragments are created.
 CC
 XX Sequence 185 AA;
 SQ

Query Match 84.6%; Score 608.5; DB 20; Length 185;
 Best Local Similarity 99.1%; Pred. No. 4e-56;
 Matches 114; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 22 PYSGPDAPGHORRVSMIDVYTRATCQPREVYVPLVTELMGTAKQLVPSCVTVVORCGC 81
 Db 1 pysgpdapghqkvkvwswldvytracqprrvvpplvtevmgtavkqlvpscvtrvqrgcg 60
 QY 82 CPDDGLECVPTGQHVMQILMIRYSSSOLGEMSLSEHSQCRCRPPKKDSAYKPD 136
 Db 61 cpddglecvptgqhvrmqilmlrlypsqjgmslehsqecrpkdsavkpd 114

RESULT 25
 AAW86218
 ID AAW86218 standard; protein; 194 AA.
 XX
 AC AAW86218;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-3 truncated fragment 1.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN W09849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX

PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 XX Bohlen P;
 XX
 XX WPI; 1999-009426/01.
 DR
 XX
 XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 XX
 PS Claim 5; Fig 2C; 113pp; English.
 XX
 XX The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia, stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAM86218 to AAM86221 represent truncated
 CC fragments of VEGF-3.
 XX
 XX Sequence 194 AA:
 SQ
 Query Match 80.5%; Score 579; DB 20; Length 194;
 Best Local Similarity 99.1%; Pred. No. 5.4e-53;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 29 PGHQKRVNSIDVYTRATCPREVVPVLYELMGTAKQLVPSCVTVQRCGCCPDGLE 88
 Db 1 pghqkxvswldvyltrctqprevvplvclmgltvakqlvpscvtvqrcgcpddgle 60
 QY 89 CVPTGQHVBMQILMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD 136
 Db 61 cvptgqhvbmqlimlirypssqlgemslsehsqcecrpkkdsavkpd 108
 RESULT 26
 AAM86214
 ID AAM86214 standard; protein; 178 AA.
 XX
 AC AAM86214;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VRF-2 truncated fragment 1.
 XX
 XX VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; VEGF-related factor; VRF; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 XX Bohlen P;
 PT

XX
 DR WPI; 1999-009426/01.
 XX
 XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 XX
 PS Claim 5; Fig 2B; 113pp; English.
 XX
 XX The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAM86214 to AAM86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).
 XX
 XX Sequence 178 AA:
 SQ
 Query Match 79.5%; Score 571.5; DB 20; Length 178;
 Best Local Similarity 99.1%; Pred. No. 3e-52;
 Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 29 PGHQKRVNSIDVYTRATCPREVVPVLYELMGTAKQLVPSCVTVQRCGCCPDGLE 88
 Db 1 pghqkxvswldvyltrctqprevvplvclmgltvakqlvpscvtvqrcgcpddgle 60
 QY 89 CVPTGQHVBMQILMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD 136
 Db 61 cvptgqhvbmqlimlirypssqlgemslsehsqcecrp-kkdsavkpd 107
 RESULT 27
 AAM86234
 ID AAM86234 standard; protein; 167 AA.
 XX
 AC AAM86234;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-B full length sequence.
 XX
 XX VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 XX Bohlen P;
 PT WPI; 1999-009426/01.
 XX

PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Claim 5; Fig 2A; 113pp; English.
XX
CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia: to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP
CC sequences from which the truncated fragments are created.
CC
SQ Sequence 167 AA;

Query Match 79.4%; Score 571; DB 20; Length 167;
Best Local Similarity 90.4%; Pred. No. 3.1e-52;
Matches 104; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 22 PVSQPDAPGHQKRVSWIDVYTRATCPREVVPVLTVELMGTVAKOLVPSCTVQRCGCG 81
Db 1 PVSGFDGSPHQKRVSWIDVYTRATCPREVVPVLTVELMGTVAKOLVPSCTVQRCGCG 60
QY 82 CPDDGELCVPTGQHQVQMQLMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 CPDGLGECVPTGQHQVQMQLMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 115

RESULT 28
AAW86208
ID AAW86208 standard; protein; 160 AA.
AC AAW86208;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human VEGF-B truncated fragment 1.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN MO9849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia

XX
PS Claim 5; Fig 2A; 113pp; English.
XX
CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86208 to AAW86213 represent truncated
CC fragments of VEGF-B.
CC
SQ Sequence 160 AA;

Query Match 76.4%; Score 549; DB 20; Length 160;
Best Local Similarity 91.7%; Pred. No. 6.1e-50;
Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 29 PGHQKRVSWIDVYTRATCPREVVPVLTVELMGTVAKOLVPSCTVQRCGCGCPDDGLE 88
Db 1 PSHGKRVSWIDVYTRATCPREVVPVLTVELMGTVAKOLVPSCTVQRCGCGCPDDGLE 60
QY 89 CVPDGOHQVQMQLMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 CVPDGLGECVPTGQHQVQMQLMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 108

RESULT 29
AAW86219
ID AAW86219 standard; protein; 189 AA.
AC AAW86219;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human VEGF-3 truncated fragment 2.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN MO9849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
PS Claim 5; Fig 2C; 113pp; English.

CC coronary collateral vessel development in cases of cardiac ischaemia; to

CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic

CC lower limb ischaemia; stroke and peripheral vascular disease); to promote

CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86218 to AAW86221 represent truncated
 CC fragments of VEGF-3.
 XX

SQ Sequence 184 AA:

Query Match 72.3%; Score 520; DB 20; Length 184;
 Best Local Similarity 99.0%; Pred. No. 8.1e-47;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 IDVYTRATCQPREVVVPLTVEIMGTAKQLVPSCTVYQRCGGCCPDGEGECVPTGQHQR 98
 |||||||
 Db 1 IDVYTRATCQPREVVVPLTVEIMGTAKQLVPSCTVYQRCGGCCPDGEGECVPTGQHQR 60

QY 99 MQIMIRYPSQSQJGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 61 mqilmirypsqjlgemslsehsqcecrpkksavkqd 98

RESULT 34

AAW86210
 ID AAW86210 standard; protein; 152 AA.

XX AAW86210;

DT 16-FEB-1999 (first entry)

DE Human VEGF-B truncated fragment 3.

XX VEGF: VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.

XX Homo sapiens.

XX WO9849300-A2.

XX 05-NOV-1998.

XX 20-APR-1998; 98WO-US07801.

XX 25-APR-1997; 97US-0842984.

XX (COLL-) COLLATERAL THERAPEUTICS.

XX Bohlen P;

DR WPI: 1999-009426/01.

XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischemia

XX Claim 5; Fig 2A; 113pp; English.

XX The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86208 to AAW86213 represent truncated
 CC fragments of VEGF-B.

XX
 SQ Sequence 152 AA:

Query Match 71.6%; Score 515; DB 20; Length 152;
 Best Local Similarity 93.9%; Pred. No. 2.2e-46;
 Matches 93; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 38 MIDVYTRATCQPREVVVPLTVEIMGTAKQLVPSCTVYQRCGGCCPDGEGECVPTGQHQR 97
 |||||||
 Db 2 MIDVYTRATCQPREVVVPLTVEIMGTAKQLVPSCTVYQRCGGCCPDGEGECVPTGQHQR 61

QY 98 MQIMIRYPSQSQJGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 62 mqilmirypsqjlgemslsehsqcecrpkksavkpd 100

RESULT 35

AAW86216
 ID AAW86216 standard; protein; 168 AA.

XX AAW86216;

DT 16-FEB-1999 (first entry)

DE Human VRF-2 truncated fragment 3.

XX VEGF: VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; VEGF-related factor; VRF; vascular permeability.

XX Homo sapiens.

XX WO9849300-A2.

XX 05-NOV-1998.

XX 20-APR-1998; 98WO-US07801.

XX 25-APR-1997; 97US-0842984.

XX (COLL-) COLLATERAL THERAPEUTICS.

XX Bohlen P;

DR WPI: 1999-009426/01.

XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischemia

XX Claim 5; Fig 2B; 113pp; English.

XX The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86214 to AAW86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).

XX Sequence 168 AA:

Query Match	71.3%;	Score 512.5;	DB 20;	Length 168;
Best Local Similarity	99.08;	Pred. No. 4.5e-46;		
Matches 97;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1.

OY	39	IDVYRATCCPRFVVYPLVLELMTGVAVALQVPSCTWYWGCGCCPDGJLGCPTGGHOVR	98
Db	1	ldvyratccgprfvvplvlelmtgvaqlvpsectvrgcgccpdgjlcvpugqnyr	60
OY	99	MOILMIRPSSQLGEMSLSEHSQCCECRPKKDSAVK	136
Db	61	mqilmlirpssqigemslsehsqcccrp-ktdsavkpd	97

RESULT 36

ID	AAW86211	standard; protein; 150 AA.
1	MA	
2	MA	
3	MA	
4	MA	
5	MA	
6	MA	
7	MA	
8	MA	
9	MA	
10	MA	
11	MA	
12	MA	
13	MA	
14	MA	
15	MA	
16	MA	
17	MA	
18	MA	
19	MA	
20	MA	
21	MA	
22	MA	
23	MA	
24	MA	
25	MA	
26	MA	
27	MA	
28	MA	
29	MA	
30	MA	
31	MA	
32	MA	
33	MA	
34	MA	
35	MA	
36	MA	
37	MA	
38	MA	
39	MA	
40	MA	
41	MA	
42	MA	
43	MA	
44	MA	
45	MA	
46	MA	
47	MA	
48	MA	
49	MA	
50	MA	
51	MA	
52	MA	
53	MA	
54	MA	
55	MA	
56	MA	
57	MA	
58	MA	
59	MA	
60	MA	
61	MA	
62	MA	
63	MA	
64	MA	
65	MA	
66	MA	
67	MA	
68	MA	
69	MA	
70	MA	
71	MA	
72	MA	
73	MA	
74	MA	
75	MA	
76	MA	
77	MA	
78	MA	
79	MA	
80	MA	
81	MA	
82	MA	
83	MA	
84	MA	
85	MA	
86	MA	
87	MA	
88	MA	
89	MA	
90	MA	
91	MA	
92	MA	
93	MA	
94	MA	
95	MA	
96	MA	
97	MA	
98	MA	
99	MA	
100	MA	

AC AAW86211;

DT 16-FEB-1999 (first entry)

DE Human VEGF-B truncated fragment 4.

KM VEGF: VEGF-vascular endothelial growth factor VEGF-related protein;
KM recombinant; truncated: gene therapy; angiogenesis; cardiac ischemia;
KM coronary; collateral vessel development; cell growth; migration; heart;
KM lower limb ischemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; vascular permeability.

OS Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlén P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2A; 113pp; English.

CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have *in vivo* and *in vitro*
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischemia; to
CC stimulate endothelial cell growth and migration *in vitro*; to treat heart
CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86208 to AAW86213 represent truncated
CC fragments of VEGF-B.

SQ Sequence 150 AA;

Query Match	Score	DB	Length
Best Local Similarity	70.1%;	504;	20;
	93.9%;	Pred. No. 3.1e-45;	

Matches 92; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	Db	Qy	Db
39	1	99	61
IDVTRATCOBRVVVVPLVLVETMGHVAKOIVPSCVTYVGGCCPDJGLCVPYGOHVR	idvtrtctgprevvplsmelmgvnyqdlvpsectyvgcgccpddglcypdgqhyr	MQILMIRYPSQLGEMSLSEHSQCECRPRKKDSAVKPD	mqilmlqypsqdgemslsehsqccerprkkesavkpd

RESULT 37

ID AAW86221 standard; protein; 179 AA.

... AAW86221;

DT 16-FEB-1999 (first entry)

DE Human VEGF-3 truncated fragment 4.

KM VEGF: VEGF: vascular endothelial growth factor; VEGF-related protein;
KM recombinant, truncated, gene therapy; angiogenesis; cardiac ischemia;
KM coronary; collateral vessel development; cell growth; migration; heart;
KM lower limb ischemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; vascular permeability.

OS Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlén P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2C; 113pp; English

CC The invention relates to truncated VPR (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VPR subunits are used to produce
CC the truncated proteins recombinantly. The truncated VPR subunits,
CC optionally expressed from gene therapy vectors, have *in vivo* and *in vitro*
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischemia; to
CC stimulate endothelial cell growth and migration *in vitro*; to treat heart
CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW862218 to AAW862221 represent truncated
CC fragments of VEGF-3.

Sequence 179 AA;

Query Match	68.7%	Score 494	DB 20	Length 179
Best Local Similarity	98.9%	Pred. No. 4.3e-44		
Matches 92; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY 44 R A T C Q P R E V V P L T V E I M G T V A K Q L V P S C V T V Q R C G G C P D D G L E C V P T G Q H Q V R M Q I L M 103

Db 1 ratcpgrevvplvtvelmgltvakqlypvcvtvgrcgccpddglecypgqhvrmqilm 60
QY 104 IRYPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 lrypsqqlgmsleehsqcecrpkksavkqd 93

RESULT 38
AAW86212
ID AAW86212 standard; protein; 147 AA.
XX
AC AAW86212;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human VEGF-B truncated fragment 5.
XX
KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KM coronary; collateral vessel development; cell growth; migration; heart;
KM lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; vascular permeability.

XX OS Homo sapiens.
XX PN W09849300-A2.
XX PD 05-NOV-1998.
XX PE 20-APR-1998; 98WO-US07801.
XX PR 25-APR-1997; 97US-0842984.
XX PA (COLL-) COLLATERAL THERAPEUTICS.
XX PI Bohlen P;
XX DR WPI; 1999-009426/01.
XX PT New truncated vascular endothelial growth factor-related protein
XX subunits - lack part of the N-terminal sequence, used to stimulate
XX angiogenesis, e.g. for treating heart disease and ischaemia

XX PS Claim 5; Fig 2A; 113pp; English.
XX CC The invention relates to truncated VRF (vascular endothelial growth
XX factor (VEGF)-related protein) subunits that have at least one amino
XX acid N-terminal to the first Cys of the core sequence deleted. Host
XX cells transfected or transfected with expression vectors containing
XX nucleic acids encoding the truncated VRF subunits are used to produce
XX the truncated proteins recombinantly. The truncated VRF subunits,
XX optionally expressed from gene therapy vectors, have in vivo and in vitro
XX angiogenic activity and are used to stimulate angiogenesis, particularly
XX coronary collateral vessel development in cases of cardiac ischaemia; to
XX stimulate endothelial cell growth and migration in vitro; to treat heart
XX disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
XX lower limb ischaemia; stroke and peripheral vascular disease); to promote
XX healing of wounds (of skin or intestines), and to increase vascular
XX permeability. Sequences AAW86208 to AAW86213 represent truncated
XX fragments of VEGF-B.

XX Sequence 147 AA;

Query Match 68.2%; Score 490; DB 20; Length 147;
Best Local Similarity 93.7%; Pred. No. 8.9e-44;
Matches 89; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 42 YTRATCPREVVVPLTVELMGTVAKOLVPSCTVYORCGCCDDDLGECYPTGQHOVRMOI 101
Db 1 ytracpgevrvvplsmelmgvkvqlypvcvtvgrcgccpddglecypgqhvrmqil 60

QY 102 LMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 lmylrypsqqlgmsleehsqcecrpkksavkpd 95

RESULT 39
AAW04824
ID AAW04824 standard; peptide; 102 AA.
XX
AC AAW04824;
XX
DT 28-APR-1997 (first entry)
XX
DE Vascular endothelial growth factor fragment #1.

XX KW Endothelial cell; proliferation; vascular endothelial growth factor; VRF;
KM VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KM vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KM embryonic development; wound healing; tissue reorganisation; antibody;
KM cancer; metastatic risk; tumour cell; mouse.

XX OS Mus musculus.
XX PN W09626736-A1.
XX PD 06-SEP-1996.
XX PE 01-MAR-1996; 96WO-US02957.
XX PR 06-DEC-1995; 95US-0569063.
XX PR 01-MAR-1995; 95US-0397651.
XX PR 06-JUN-1995; 95US-0469427.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX DR WPI; 1996-412582/41.
XX DR N-PSDB; AAT37909.

XX PT Vascular endothelial growth factor VEGF-B proteins - useful to
XX accelerate angiogenesis in wound healing, also related nucleic acid
XX PT and antibodies for cancer diagnosis
XX PS Claim 18; Page 53-54; 107pp; English.

XX CC AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
XX proteins of the invention, which promote endothelial or mesodermal cell
XX proliferation. VEGF is also a glycosylated cationic dimer, and is
XX sometimes referred to as vascular permeability factor (VPF). VEGF has
XX diverse effects, depending on the specific biological context in which
XX it is found. VEGF is a potent endothelial cell mitogen, and directly
XX contributes to induction of angiogenesis in vivo by promoting
XX endothelial cell growth during normal embryonic development, wound
XX healing, and tissue regeneration/reorganisation. The VEGF proteins of
XX the invention share the angiogenic and other properties of VEGF, but are
XX distributed and expressed in tissues differently to VEGF. The proteins
XX can therefore be used to accelerate angiogenesis in wound healing.
XX Antibodies against the proteins can be used for inhibiting angiogenesis.
XX The antibodies can also be used diagnostically to quantitatively detect
XX VEGF-B. Primers complementary to the coding sequences for the proteins
XX of the invention can also be used to detect VEGF-B coding sequences.
XX Quantification of VEGF-B in cancer biopsy specimens may be useful as an
XX indicator of metastatic risk. VEGF-B expression in a cell can be
XX retarded using antisense sequences direct against the VEGF coding
XX sequences; this is especially useful in retarding VEGF expression in
XX tumour cells.

XX Sequence 102 AA;

Query Match 68.0%; Score 489; DB 17; Length 102;

Best Local Similarity 91.8%; Pred. No. 7.3e-44;
Matches 89; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

0Y      33 KKVSWIDVYTRATCPREVVNVELTVELMGTVAKOLVPSCVTYQRCGGCCPDDGLECVPT 92
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 rpvwpwidvaratcqbrevnvvglsmelmgnvkvqlvpscvtlvrgcgccpddglecvpt 61

```

```
QY 93 GQHVRMQIIMIRPSSQLGEMSLSEHSQCCECRPKK 12
      |||||:|||||
Db 62 gqhqymqilmiqypssqlgemslsehsqcecrpkk 98
```

RESULT 40
AAW80488
ID AAW80488 standard; Protein; 102 AA.

DT 29-JAN-1999 (first entry)

DE Murine vascular endothelial growth factor (VEGF)-B.

KM Vascular endothelial growth factor; VEGF; proliferation; mouse;
endothelial cell; angiogenesis; tissue growth; organ repair.

OS Mus sp.

PN US5840693-A.

PD 24-NOV-1998.

PF 01-MAR-1996; 96US-0609443.

PR 01-MAR-1996; 96US-0609443.

PR 06-JUN-1995; 95US-0469427.

XX

PA (UYHE-) UNIV HELSINKI LICENS

PI Alitalo K, Eriksson U, Olofsson B, I

DR WPI; 1999-034079/03.

XX

PT them - useful for im

XX

PS Claim 1; Fig 1; 52pp; English.

CC The present sequence represents murine vascular endothelial growth factor

reading frames. The proteins are used for promoting proliferation of endothelial cells and for stimulating angiogenesis (the proliferation of new capillaries form pre-existing blood vessels). These activites are useful for treating tissue growth and repair, including organ repair. This is also useful in pregnancy, in follicle development, as these processes must occur in development of the placenta. The proteins can also be used to raise antibodies, either for use in detection of the proteins or as inhibitors of their action. This is especially useful as angiogenesis is required by tumours as they need new blood supplies to grow and proliferate.

SQ Sequence 102 AA;

Query Match	68.08; Score 489; DB 20; Length 102;
-------------	--------------------------------------

```
Db      2 rpvpvpidyaratcqprevvvplsmelmgnvvkqlvpscvrvqrcgacpcddglecvpt 61
```

```

Oy  93 GQHOVMOILMIRYPSQSOLGENSLSEHSQCECRPKKK 129
      | | | | | | | | | | | | | | | | | | | | | |
Db  62 gqhqymqilmiqypsqqlgensleehsgcecrpkkk 98

```

RESULT 41
AAW86217
ID AAW86217 standard; protein; 163 AA

DT 16-FEB-1999 (first entry)

Human VRF-2 truncated fragment 4.

KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;

KW coronary; col

KW wound healing

OS Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL T

PI Bohlen P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS
 PS Claim 5; Fig 2B; 113bp; English.
 XX
 CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia), stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestine), and to increase vascular
 CC permeability. Sequences AAM86214 to AAM86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).

SQ Sequence 163 AA;

Query Match	67.7%	Score 486.5;	DB 20;	Length 163;
Best Local Similarity	98.9%	Pred. No. 2.3e-43;		
Matches 92;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

```
OY      44 RATCQPREVVNPLTVELMGSTVAKQLVPSCYTVQRGGCCPDDGLCYPTGQHVRMQLIM 10
|||||
|||||
Db      1 ratcgprevvnlptvelmgstvakqlvpscvtvgqrgccppddglcycptgqhvrmlim 60
```

QY 104 IRYPSQGLGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||
 DB 61 IRYPSQGLGEMSLSEHSQCECRP-KKDSAVKPD 92

RESULT 42

AAW86213
 ID AAW86213 standard; protein; 145 AA.

AC AAW86213;

DT 16-FEB-1999 (first entry)

DE Human VEGF-B truncated fragment 6.

KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 coronary; collateral vessel development; cell growth; migration; heart;
 lower limb ischemia; stroke; peripheral vascular disease; intestine;
 wound healing; skin; vascular permeability.

OS Homo sapiens.

PN MO9849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlen P;

DR WPI: 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein
 subunits - lack part of the N-terminal sequence, used to stimulate
 angiogenesis, e.g. for treating heart disease and ischemia

PS Claim 5; Fig 2A; 113pp; English.

CC The invention relates to truncated VRP (vascular endothelial growth
 factor (VEGF)-related protein) subunits that have at least one amino
 acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia, stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86208 to AAW86213 represent truncated
 CC fragments of VEGF-B.

CC Sequence 145 AA;

Query Match

Best Local Similarity 66.5%; Score 478; DB 20; Length 145;

Matches 87; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 44 RATCPREVVPVTVELMGTVAKOLVPCVTVQRCGCCPDGLGECVPTGQHOVRMOILM 103
 |||||

DB 1 ratcqvrevvvpjlmelmgnvkvqlypscvtvgrcgscpddglecvptgqbvmqilm 60

QY 104 IRYPSQGLGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||

DB 61 IRYPSQGLGEMSLSEHSQCECRPKKDSAVKPD 93

RESULT 43

AAV33440
 ID AAV33440 standard; Protein; 190 AA.

AC AAV33440;

DT 13-DEC-1999 (first entry)

DE Parapox virus VEGF growth factor homologue protein fragment 7.

KW D1701; Vascular endothelial growth factor; PPV-VEGF; angiogenesis;
 endothelial cell proliferation; gene therapy; diagnostic; tissue repair;
 immunomodulation; dendritic cell differentiation; DNA vaccine.

OS Parapoxvirus.

PN DE19813774-A1.

PD 30-SEP-1999.

PF 27-MAR-1998; 98DE-1013774.

PR 27-MAR-1998; 98DE-1013774.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Dehio C, Roettgen M, Rziha H, Buettner M;

DR WPI: 1999-552202/47.

PT Homolog of human vascular endothelial growth factor useful for
 stimulating endothelial cell proliferation, e.g. for stimulating
 angiogenesis or tissue repair or for immunomodulation

PS Disclosure; Fig 2; 16pp; German.

CC This invention describes a novel polypeptide that is a parapox virus
 CC homolog of human vascular endothelial growth factor (PPV-VEGF) and
 CC stimulates endothelial cell proliferation. The products of the invention
 CC have angiogenic activity. The polypeptide can be used in pharmaceutical
 CC compositions for therapeutic or diagnostic use, e.g. for stimulating
 CC angiogenesis or tissue repair or for immunomodulation, e.g. by
 CC stimulating endothelial cell proliferation or inhibiting dendritic cell
 CC differentiation. Nucleic acids encoding the polypeptide can be used in
 CC pharmaceutical compositions for DNA vaccination or gene therapy. This
 CC sequence represents a protein fragment of a parapox virus D1701 vascular
 CC endothelial growth factor (VEGF) homologue.

CC Sequence 190 AA;

Query Match

Best Local Similarity 37.6%; Score 270.5; DB 20; Length 190;

Matches 55; Conservative 22; Mismatches 42; Indels 3; Gaps 2;

QY 10 LAILQLAPAOAPVSOQDPAGHOR--KVWSMIDVYRATCOPREVVPVTVELMGTVAKO 67
 |||||

DB 12 laillylhaksgqaemaegdkphvkvfmvqyqrsyrcrptctvdlfgeydeiey1 71

QY 68 LVPSCTVQRCGCCCPDGLGECVPTGQHOVRMOILMIR-YPSQGLGEMSLSEHSQCECRP 126
 |||||

DB 72 fkpvcplmrcgscndeglecvpteeftmgtmrlkphgqghgmsflqhnkccrpp 131

QY 127 KK 128

DB 132 KK 133

RESULT 44

AAK22348
 ID AAK22348 standard; Protein; 146 AA.

```

XX AAR22348;
AC
XX
XX 29-JUL-1992 (first entry)
DT
XX
XX Alternative form of VEGF mature A-subunit with 120 amino acids.
DE
XX
XX Rat glioma cell; GS-9L; conditioned medium; heterodimer; VEGF-11;
KM homodimer; mitogenesis; vascular repair; blood vessel implant;
KM polymerase chain reaction; alternative splicing.
XX
XX Rattus.
OS
XX
XX Key 1.26 location/Qualifiers
FH Peptide /label= signal
FT Protein /label= VEGF_A-subunit
FT /note= "120 amino acids long"
FT
XX
XX EP476983-A.
PN
XX
XX 25-MAR-1992.
PD
XX
XX 18-SEP-1991; 91EP-0308489.
PF
XX
XX 21-SEP-1990; 90US-0586640.
PR 21-SEP-1990; 90US-0586638.
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Bayne ML, Conn GL, Thomas KA;
PI
XX
XX WPI; 1992-098641/13.
DR N-PSDB; AAQ23039.
DR
XX
XX Vascular endothelial cell growth factor II - used as coating for
PT artificial blood vessels or to promote tissue repair
PT
XX
XX Example 9; Page 14 and Fig 4; 38pp; English.
PS
XX
XX Multiple cDNAs encoding alternative forms of the VEGF A-subunit
CC were amplified using PCR primers as in AAQ23049 and AAQ23050. Three
CC sets of clones were identified. Clone #12 encoded the 164 amino acid
CC secreted form of VEGF A-subunit (see AAR22347). Clone #14 has a 135 bp
CC deletion and thus encodes a 120 amino acid form and Clone #16 has a
CC 72bp insertion and encodes a 188 amino acid mature protein (AAR22351).
CC The deleted region lies between the second base of the Asn140 codon
CC and the third base of the Arg184 codon. The 120 amino acid mature
CC protein has Asn140 converted to Lys140.
CC See also AAQ23038-Q23059.
XX
XX
XX Sequence 146 AA;
SQ

```

```

Query Match 37.5%; Score 269.5; DB 13; Length 146;
Best Local Similarity 43.8%; Pred. NO. 1.4e-20;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

```

```

QY 10 LAALLQLAPADVPSPDAPGHQR--KVVSMIDVYTRATCPREVVVPLVTELNGTVAKQ 67
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 lallllylhakwsgaqrtegeqkavevkvfmdyqrgyscrptletlvdifgeydeleyl 71
QY 68 LVPSCTVYVQRGGCCPDGGLCVPTGQHVRMQLIMIR-YSSQLGEMSLSEHSQCCECRP 126
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 72 fkpvcvplmrcaagcndealectvpsnvvmqlmrkphsqhlgemsflqhsrccr 131
QY 127 KKKSAAVAPD 136
  || : || :
DB 132 kk--drtkpe 139

```

RESULT 45

```

AAR27354
ID AAR27354 standard; Protein; 146 AA.
XX
XX AAR27354;
AC
XX
XX 25-FEB-1993 (first entry)
DT
XX
XX Sequence of vascular endothelial cell growth factor VEGF A
DE 146 amino acid residue subunit.
DE
XX
XX Vascular development; mitogen; blood vessel;
KM vascular endothelial growth factor; neovascularisation.
KM
XX
XX Rattus.
OS
XX
XX EP506477-A.
FN
XX
XX 30-SEP-1991.
PD
XX
XX 27-MAR-1992; 92EP-0302750.
PF
XX
XX 28-MAR-1991; 91US-0676436.
PR
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Bayne ML, Thomas KA;
PI
XX
XX WPI; 1992-325745/40.
DR N-PSDB; AAQ28953.
DR
XX
XX Vascular endothelial cell growth factor sub-units - which stimulate
PT vascular endothelial cell growth, used for inducing tissue repair
PT and growth.
XX
XX Disclosure; Fig 4; 61pp; English.
PS
XX
XX The full length coding region of the A subunit or monomer of VEGF
CC is determined from three sets of overlapping cDNA clones. Degenerate
CC oligo. primers based on the amino acid sequences
CC Phe-Met-Asp-Val-Tyr-Gln from polypeptide 142 (residues 42-47) and
CC Cys-Lys-Asn-Thr-Asp from polypeptide 138 (residues 164-168) were used
CC to PCR amplify the central region of the cDNA for VEGF A chain.
CC A single band migrating at 420 bp was gel purified, digested with SalI,
CC ligated into pGEM32f(+) and sequenced. The nucleotide sequence
CC obtained (p4238) was used to design antisense and sense PCR primers
CC to amplify the 5' and 3' ends of the cDNA. These 5' and 3' clones
CC are denoted p5-15 and pW3, respectively. In addition to the cDNA
CC coding the 164 amino acid secreted form identified by protein
CC sequencing, two alternatively spliced cDNAs encoding a 146 amino acid
CC and a 214 amino acid forms are cloned and sequenced.
XX
XX
XX Sequence 146 AA;
SQ

```

```

Query Match 37.5%; Score 269.5; DB 13; Length 146;
Best Local Similarity 43.8%; Pred. NO. 1.4e-20;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

```

```

QY 10 LAALLQLAPADVPSPDAPGHQR--KVVSMIDVYTRATCPREVVVPLVTELNGTVAKQ 67
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 lallllylhakwsgaqrtegeqkavevkvfmdyqrgyscrptletlvdifgeydeleyl 71
QY 68 LVPSCTVYVQRGGCCPDGGLCVPTGQHVRMQLIMIR-YSSQLGEMSLSEHSQCCECRP 126
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 72 fkpvcvplmrcaagcndealectvpsnvvmqlmrkphsqhlgemsflqhsrccr 131
QY 127 KKKSAAVAPD 136
  || : || :
DB 132 kk--drtkpe 139

```

Search completed: September 10, 2002, 02:49:15

Job time: 3708 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 01:51:32 ; Search time 43.52 Seconds
(without alignments)
300.279 Million cell updates/sec

Title: US-09-912-436-6
Perfect score: 719
Sequence: 1 MSPLLRRLLLALLQLAPAQ.....EEHSQCECRPKKDSAVKPD 136
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	89.6	188	2 JC4680	vascular endotheli
2	644	89.6	207	2 JC4679	vascular endotheli
3	270.5	37.6	190	2 S52130	vascular endotheli
4	269.5	37.5	190	2 A35987	glioma-derived vas
5	267.5	37.2	190	2 B44881	vascular endotheli
6	267.5	37.2	214	2 A44881	vascular endotheli
7	266.5	37.1	190	2 B40080	vascular endotheli
8	264	36.7	232	2 A41551	vascular endotheli
9	263.5	36.6	146	2 S57956	ovine vascular end
10	253.5	35.3	120	2 A33787	vascular endotheli
11	199.5	27.7	133	2 B49530	vascular endotheli
12	187.5	26.1	149	2 A41236	placental growth f
13	179.5	25.0	128	2 T51295	vascular endotheli
14	176	24.5	158	2 A56125	vascular endotheli
15	145.5	20.2	148	2 D49530	16k vascular endot
16	145	20.2	419	2 S69207	vascular endotheli
17	129	17.9	211	1 PFH0G1	platelet-derived g
18	127.5	17.7	166	2 JN0248	platelet-derived g
19	127.5	17.7	198	2 J50735	platelet-derived g
20	127	17.7	196	2 B28964	platelet-derived g
21	127	17.7	197	2 S25096	platelet-derived g
22	126	17.5	245	1 TVCTSS	platelet-derived g
23	126	17.5	196	2 A37359	platelet-derived g
24	123	17.1	226	1 TVMVS	PDGF-related trans
25	123	17.1	241	1 S08220	platelet-derived g
26	119.5	16.6	215	2 S08220	platelet-derived g
27	119	16.6	200	2 I51551	platelet-derived g
28	119	16.6	226	2 I51550	platelet-derived g
29	117.5	16.3	196	2 A48851	platelet-derived g

30	114.5	15.9	225	2 S25097	platelet-derived g
31	114	15.9	241	1 PMSGB	platelet-derived g
32	111	15.4	271	2 A25669	PDGF-related trans
33	95.5	13.3	370	2 JC7592	spinal cord-derive
34	85.5	11.9	370	2 JC7591	spinal cord-derive
35	78	10.8	378	2 S72599	hypothetical prote
36	77.5	10.8	335	2 T31561	hypothetical prote
37	76	10.6	452	2 A12071	hypothetical prote
38	75.5	10.5	335	2 T31560	hypothetical prote
39	75	10.4	188	2 AG0273	probable iron-sulf
40	75	10.4	335	2 T31559	hypothetical prote
41	74	10.3	293	2 T31840	hypothetical prote
42	74	10.3	519	2 D70695	hypothetical prote
43	73.5	10.2	1416	2 E88550	protein ZC84.1 (im
44	73.5	10.2	2844	2 S28291	hypothetical prote
45	72.5	10.1	249	2 T21785	hypothetical prote

ALIGNMENTS

```
RESULT 1
JC4680      vascular endothelial growth factor-related factor 167 precursor - mouse
N:Alternate names: VRF 167 protein
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C:Accession: JC4680
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A>Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052
A:Accession: JC4680
A:Molecule type: mRNA
A:Residues: 1-188 <TOM>
A:Cross-references: GB:U43837; NID:G1314335; PIDN:AAC52553.1; PID:G1314336
A:Comment: This factor is a mitogen, that is selective for endothelial cells, and bel
ar endothelial growth factors 167 and VEGF 186.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Introns: 137/2
F:1-21/Domain: signal sequence #status predicted <Sig>
F:22-188/Product: vascular endothelial growth factor-related factor #status predicted

Query Match      89.6%; Score 644; DB 2; Length 188;
Best local similarity 89.0%; Pred. No. 2.2e-55;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSPLLRRLLLALLQLAPAQAVSQPDAGRHGRKRVSVTDYTRATCOPREVVPFLYTEL 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 MSPLLRRLLLALLQLAPQAVSQPDGSHQKRVPMVDVYARATCOPREVVPFLSMEL 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 61 MCTVAKQVLVSCVTYQRCGGCCPDGDLCEVPYQGHQVRMQIIMIRPSSQLEMSLEERS 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 61 MGNVYKQVLVSCVTYQRCGGCCPDGDLCEVPYQGHQVRMQIIMIRPSSQLEMSLEERS 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 121 QCECRPKKDSAVKPD 136
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 121 QCECRPKKDSAVKPD 136
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 2
JC4679      vascular endothelial growth factor-related factor 186 precursor - mouse
N:Alternate names: VRF 186 protein, VEGF 186
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C:Accession: JC4679
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A>Title: Characterization of the murine VEGF-related factor gene.
```

A:Reference number: JC4679; MUID:96183052
A:Accession: JC4679
A:Molecule type: mRNA
A:Residues: 1-207 <TOW>
A:Cross-references: GB:043836; NID:g1703480; PIDN:AAC52932.1; PID:g1314334
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the endothelial growth factors 167 and 186.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Keywords: growth factor
F.1-21/Domain: signal sequence #status predicted <Sig>
F.22-207/Product: vascular endothelial growth factor related factor #status predicted <Sig>

Query Match 89.6%; Score 644; DB 2; Length 207;
Best Local Similarity 89.0%; Pred. No. 2.4e-55;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 NSPLRLRLALALALQAPAPVSDAPAGHQRKVVSMIDVYTRATCOPREVVYPLTEL 60
DB 1 NSPLRLRLALALQAPAPVSDAPAGHQRKVVSMIDVYTRATCOPREVVYPLTEL 60
QY 61 MGVAKQLVPSCVTVQRCGGCCPDGDLCEVPTGQHVRMQILMIRYPSQSGEMSEHS 120
DB 61 MGVAKQLVPSCVTVQRCGGCCPDGDLCEVPTGQHVRMQILMIRYPSQSGEMSEHS 120
QY 121 QCECRPKKKDSAVKPD 136
DB 121 QCECRPKKKDSAVKPD 136

RESULT 3
SS2130
vascular endothelial growth factor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: SS2130
R:Sharma, H.S.; Tang, Z.H.; Cho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth factor
A:Reference number: SS2130; MUID:95143284
A:Accession: SS2130
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <SHA>
A:Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 37.6%; Score 270.5; DB 2; Length 190;
Best Local Similarity 45.1%; Pred. No. 4.7e-19;
Matches 53; Conservative 22; Mismatches 42; Indels 3; Gaps 2;

QY 10 LAALLQLARPAQAPVSDAPAGHQR--KVVSMIDVYTRATCOPREVVYPLTELMTGTVAKQ 67
DB 12 LALLLLYLNHAKKQAAPRAEAGDQKPEHYVKKEMDYQRYSCRIETLVIPDEYDEIYI 71
QY 68 LVPSCVTVQRCGGCCPDGDLCEVPTGQHVRMQILMIR-YPSSQSGEMSEHSQCECRP 126
DB 72 FKPSCVPLMRGCGCCNDGELCEVPTGQHVRMQILMIR-YPSSQSGEMSEHSQCECRP 131
QY 127 KK 128
DB 132 KK 133

RESULT 4
A35987
glioma-derived vascular endothelial cell growth factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C:Accession: A35987
C:Comment: G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope,

[illegible]


```

A:Accession: A40454
A:Molecule type: DNA
A:Residues: 1-165,183-232 <RT1>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GB:M63977; GB:M63978
A:Molecule type: DNA
A:Residues: 1-140,'N',183-232 <RT12>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GB:M63977; GB:M63978
A:Accession: C40454
A:Molecule type: DNA
A:Residues: 1-141,227-232 <RT13>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GB:M63977; GB:M63978
R:Kleck, P.J.; Hauser, S.D.; Krivy, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.T.
Science 246, 1309-1312, 1989
A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A:Reference number: A40079; MUID:90069609
A:Accession: A40079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-165,183-232 <REC>
A:Cross-references: GB:M27281; NID:9340300; PIDN:AAA36807.1; PID:9340301
R:Leung, D.W.; Cachianes, G.; Kiang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A:Reference number: A40080; MUID:90069608
A:Accession: A40080
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140,'N',183-232 <LEU>
A:Cross-references: GB:M2977; NID:9181970; PIDN:AAA35789.1; PID:9181971
R:Weinhold, K.; Martne, D.; Welch, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial
A:Reference number: JQ1463; MUID:92231879
A:Accession: JQ1463
A:Molecule type: mRNA
A:Residues: 1-140,'N',183-232 <WEI>
A:Cross-references: EMBL:X62568; NID:937658; PIDN:CAA44447.1; PID:937659
A:Experimental source: AIDS-Kaposi's sarcoma cell
A:Accession: JQ1464
A:Molecule type: mRNA
A:Residues: 1-140,'N',227-232 <ME2>
A:Experimental source: AIDS-Kaposi's sarcoma cell
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay
J. Biol. Chem. 264, 20017-20024, 1989
A:Title: Human vascular permeability factor. Isolation from U937 cells.
A:Reference number: A34492; MUID:90062112
A:Accession: A34492
A:Molecule type: protein
A:Residues: 27-36;43-49,'R',72-76,'Q',78-81;59-71 <CON>
A:Comment: The most common of several alternatively spliced forms is VEGF 165.
C:Genetics:
A:Gene: GDB:VEGF
A:Cross-references: GDB:132244; OMIM:192240
A:Map position: 6p21-6p12
C:Function:
A:Description: Promotes fluid and protein leakage from blood vessels
C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro
F:1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20
F:1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predic
F:1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predic
F:1-26/Domains: signal sequence #status predicted <SIG>
F:101/Binding site: carbohydrate (asn) (covalent) #status predicted

```

```

Query Match 36.7%; Score 264; DB 2; Length 232;
Best Local Similarity 43.9%; Pred. No. 2.4e-18;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

```

```

Oy 10 LAALLQLAPAPVSGPPAPG---HQRKVSMDVYTRATCOPREVVPPLVTELMGTAK 66
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 LALLLYLHNAKWSQAPAPAEAGGQNHHEVYKMDVYQSRYPETLVDFQEPDELEY 71

```

```

Oy 67 QLVPSCVTVQRCGCCPDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECR 125
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 IFKPSCVPLMRGCGCCNDEGECVPTESNITMQIMRIKPHOGHIGEMSLQHNKCECR 131
Oy 126 PKK 128
| | |
Db 132 PKK 134

```

RESULT 9

S57956

ovine vascular endothelial growth factor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999

C:Accession: S57956

R:Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.

submitted to the EMBL Data Library, July 1995

A:Reference number: S57956

A:Accession: S57956

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-146 <RED>

A:Cross-references: EMBL:X89506; NID:9899350; PIDN:CAA61677.1; PID:9899351

```

Query Match 36.6%; Score 263.5; DB 2; Length 146;
Best Local Similarity 44.3%; Pred. No. 1.8e-18;
Matches 54; Conservative 23; Mismatches 42; Indels 3; Gaps 2;

```

```

Oy 10 LAALLQLAPAPVSGPPAPGHR--KYVSMIDVYTRATCOPREVVPPLVTELMGTAKQ 67
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 LALLLYLHNAKWSQAPAPAEAGGQKPEHVKEMDVYQSRYPETLVDFQEPDELEY 71
Oy 68 LVPSCVTVQRCGCCPDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECRP 126
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 FKPSCVPLMRGCGCCNDESLCEVPTSEFNITMQIMRIKPHOSQHIGEMSLQHNKCECRP 131
Oy 127 KK 128
| |
Db 132 KK 133

```

RESULT 10

A33787

vascular endothelial growth factor (version 1) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999

C:Accession: A33787

R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr

Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989

A:Title: Vascular endothelial growth factor: a new member of the platelet-derived gro

A:Reference number: A33787; MUID:90121225

A:Accession: A33787

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <RTS>

A:Cross-references: GB:M33750; NID:9163810; PIDN:AAA30805.1; PID:9163811

C:Keywords: alternative splicing

```

Query Match 35.3%; Score 253.5; DB 2; Length 120;
Best Local Similarity 46.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 34; Indels 3; Gaps 2;

```

```

Oy 26 PDAPGHQR--KYVSMIDVYTRATCOPREVVPPLVTELMGTAKQLVPSCVTVQRCGCCP 83
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 PMAEGGQKPEHVKEMDVYQSRYPETLVDFQEPDELEYFKPSCVPLMRGCGCN 61
Oy 84 DDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECRPK 128
| : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 DESLECVPTSEFNITMQIMRIKPHOSQHIGEMSLQHNKCECRPK 107

```


A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <L>T>
A:Cross-references: GB:S67522; NID:q456900; PIDN:AA29223.1; PID:q456902
A>Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBI:P.141426)

Query Match 20.2%; Score 145.5; DB 2; Length 148;
Best Local Similarity 30.5%; Pred. No. 5.4e-07;
Matches 39; Conservative 23; Mismatches 53; Indels 13; Gaps 4;

QY 7 RLILALILAPAPAPVSDP-DAPGHQRKVVSMIDVYTRATPCOREVYVPLTVELMGTVA 65
Db 8 QVVVALILICMNIPECVSOSNDSPPTN---DMNRILDKSGCKPRDVTYVILGEYPESTN 64
QY 66 KOLVPSCVTYVORCGGCCPDGLLEC--VPTGOHVQMOILMIRYP-----SSQLGEMSL 116
Db 65 LQYNPRCVTYKRCSCGCGNGGQICTANETNRTYTVSVTGVSSSGTNGSVTNLQRIISV 124
QY 117 EHSQCEC 124
Db 125 TEHTKDC 132

RESULT 16

S69207
vascular endothelial growth factor C precursor - human
N:Alternate names: FLT4 ligand DHM
C:Species: Homo sapiens (man)
C>Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C:Accession: S69207; S61795; S71443; S69208; G02659
R:Joukov, V.; Pejusola, K.; Kaipainen, A.; Chillov, D.; Lahtinen, I.; Kuk, E.; Sakela, EMO J. 15, 1751, 1996
A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for A:Reference number: S69207; MUID:96203094
A:Accession: S69207
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <D>U>
A:Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118200
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A>Note: this is a revision to the sequence from reference S61795
R:Joukov, V.; Pejusola, K.; Kaipainen, A.; Chillov, D.; Lahtinen, I.; Kuk, E.; Sakela, EMO J. 15, 290-298, 1996
A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the FLT4 (V A:Reference number: S61795; MUID:96178224
A:Accession: S61795
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 70-419 <D>U1>
A>Note: this sequence has been revised in reference S69207
A:Accession: S71443
A:Molecule type: protein
A:Residues: 'X', 104-120 <D>U2>
R:Lee, J.; Gray, A.; Yuan, J.; Luo, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A:Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp A:Reference number: S69208
A:Accession: S69208
A:Molecule type: mRNA
A:Residues: 1-419 <L>E>
A:Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA65214.1; PID:g1150989
R:Morris, J.C.
submitted to the EMBL Data Library, May 1996
A:Accession: G02659
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-419 <M>R>
A:Cross-references: EMBL:U58111; NID:g1373426; PIDN:AA202909.1; PID:g1373427
C:Genetics:
A:Gene: GDB:VEGFC; VRP

A:Cross-references: GDB:3890883; OMIM:601528
F:1-12/Domain: signal sequence #status predicted <SIG>
F:13-102/Domain: propeptide #status predicted <PRO>
F:103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 20.2%; Score 145; DB 2; Length 419;
Best Local Similarity 32.7%; Pred. No. 1.6e-06;
Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

QY 28 APGHQRKVVSMIDVYTRAT-COPREVYVPLTVELMGVAKOLVPSCVTYVORCGGCCPDG 86
Db 111 AAHTNTEILKSIDENRKTICMPREVCIDYKRGVATNTFFRPVSVTRCGCCNSEG 170
QY 87 LECVPTGOHVQMOILMIRYPSOLGE--MSLEHSQCECRPK 127
Db 171 LQCMNTSTYLSKTLFEITVPLSGPRPVITSFANHSCCMK 214

RESULT 17

PFHUG1

platelet-derived growth factor chain A precursor - human
N:Alternate names: PDGF A-chain; PDGF-A; platelet-derived growth factor 1
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Feb-2000
C:Accession: A28964; S47564; A42002; A01379; S00173; A28122
R:Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A:Title: Platelet-derived growth factor A chain: gene structure, chromosomal location A:Reference number: A28964; MUID:8814463
A:Accession: A28964
A:Molecule type: DNA
A:Residues: 1-211 N>
A:Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987; R:Yakimoto, Y.; Kuramoto, A.
Biochim. Biophys. Acta 1222, 511-514, 1994
A:Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth A:Reference number: S47564; MUID:94312450
A:Accession: S47564
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <T>K>
R:Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A:Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF A:Reference number: A42002; MUID:92307656
A:Accession: A42002
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 152-211 O2>
R:Betscholtz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urduea, M.S.; E Nature 320, 695-699, 1986
A:Title: cDNA sequence and chromosomal localization of human platelet-derived growth A:Reference number: A01379; MUID:86203630
A:Accession: A01379
A:Molecule type: mRNA
A:Residues: 1-211 E>
A:Cross-references: GB:X03795; NID:q35365; PIDN:CAA27421.1; PID:q35366
A:Experimental source: clonal glioma cell line U-343 MG8C12:6, a tumor cell line EHS Lett. 223, 243-246, 1987
R:Hoppe, J.; Schumacher, I.; Eichner, W.; Welch, H.A.
A:Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distant A:Reference number: S00173; MUID:88030061
A:Accession: S00173
A:Molecule type: mRNA
A:Residues: 1-193 'DVR' <H>P>
A:Cross-references: EMBL:X06374; NID:q35363; PIDN:CAA29677.1; PID:q35364
R:Roisman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betscholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A:Title: Structural characterization of the human platelet-derived growth factor A-ch A:Reference number: A28122; MUID:88174698
A:Accession: A28122
A:Molecule type: mRNA

C>Date: 09-Oct1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C:Accession: J50735
R:Nakamura, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki,
Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A>Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vasculature.
A:Reference number: JN0248; MUID:92246970
A:Accession: J50735
A:Molecule type: mRNA
A:Residues: 1-198 <NMK>
A>Note: this protein corresponds to the endothelial type of human A chain
C:Superfamily: platelet-derived growth factor
F:1-20/Domain: signal sequence #status predicted <SIG>
E:21-89/Domain: propeptide #status predicted <PRO>
F:90-198/Product: platelet-derived growth factor A1 chain #status predicted <MAT>

Query Match 17.7%; Score 127.5; DB 2; Length 198;
Best Local Similarity 30.1%; Pred. No. 4e+05;
Matches 34; Conservative % 24; Mismatches 46; Indels 9; Gaps 5;

OY 19 AAAPSPDAPGCHOKRVSMIDVTRATCPREV--VPPLVELMGIVAKOLY-PSCVTY 75
 :| | | :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 71 ARHVAKEPPAPVPAVRKRRT-IEEALPAICKRTVIYEIPRS-QVDPTSANFLIMPCVEV 128

OY 76 ORGGCCPDGEGCVTGQHQVMQILMIR----PSSQLGEMLSEHSOEC 124
 ::|||::|::|:|::|::|::|::|::|::|::|::|::|:
DB 129 KRCTGCCTTSSVKCPFSRHHRSVAKAVEYRKPKLKEOVRLHELEAC 181

RESULT 20
B28964
platelet-derived growth factor chain A precursor splice form 2 - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: B28964; B42002; B28122
R:Bonthron, D.T.; Collins, T.G.; Grzeschik, K.H.; van Roy, N.; Speleman, F.,
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A>Title: Platelet-derived growth factor A chain: gene structure, chromosomal location
A:Reference number: A28964; MUID:88144463
A:Accession: B28964
A:Molecule type: DNA
A:Residues: 1-196 <BOH>
A:Cross-references: GB:M1571; GB:I03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987;;
R:Bonthron, D.; Collins, T.G.; Grzeschik, K.H.; van Roy, N.; Speleman, F.,
Genomics 13, 257-263, 1992
A>Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF
A:Reference number: A42002; MUID:92307656
A:Accession: B42002
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 152-196 <BO2>
R:Roosman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.,
Mol. Cell. Biol. 8, 571-577, 1988
A>Title: Structural characterization of the human platelet-derived growth factor A-chain
A:Reference number: A28122; MUID:88174698
A:Accession: B28122
A:Molecule type: mRNA
A:Residues: 1-63,'TRD','67-196 <ROK>
A:Cross-references: GB:M20488
A>Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 66
C:Comment: Exon 6 is spliced out of this variant splice form. For the major splice form
C:Genetics:
A:Gene: GDB:PDGFA
A:Cross-references: GDB:J20266; OMIM:173430
A:Map position: 7p22-7p22
C:Superfamily: platelet-derived growth factor
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet

Query Match 17.7%; Score 127; DB 2; Length 196;
Best Local Similarity 30.3%; Pred. No. 4.4e+05;
Matches 30; Conservative 22; Mismatches 35; Indels 12; Gaps 5;

QY 103 MIR-----YPSOIGEMSLSEHSEC 124
 Db 137 QVRKEIVRKRPFRKATVLEDLACKC 165

RESULT 25
 PFHUG2
 platelet-derived growth factor chain B precursor [validated] - human
 N;Alternate names: PDGF B-chain; PDGF-B; PDGF-II; PDGF-related transforming protein (sis
 C;Species: Homo sapiens (man)
 C;Date: 18-Apr-1984 #sequence, revision 20-Sep-1984 #text, change 08-Dec-2000
 C;Accession: A94276; A21024; A23532; A93366; A25141; A94271; A93308; A43499; S56115; 157
 C;Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz, M.S.; Wong-Staal, F.
 Science 225, 636-639, 1984
 A;Title: Transforming potential of human c-sis nucleotide sequences encoding platelet-de
 A;Reference number: A94276; MUID:84250225
 A;Accession: A94276
 A;Molecule type: DNA
 A;Residues: 1-241 <JOS1>
 A;Cross-references: GB:K01401; NID:G338206; PIDN:AAA60552.1; PID:G338209
 R;Chiu, I.M.; Reddy, E.P.; Givol, D.; Robbins, K.C.; Tronick, S.R.; Aaronson, S.A.
 Cell 37, 123-129, 1984
 A;Title: Nucleotide sequence analysis identifies the human c-sis proto-oncogene as a str
 A;Reference number: A21024; MUID:84205633
 A;Accession: A21024
 A;Molecule type: DNA
 A;Residues: 17-20, 'RQ', 22-241 <CHT>
 A;Cross-references: GB:K01917; NID:G338197
 R;Proc, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 2392-2396, 1986
 A;Title: Structure and sequence of the human c-sis/platelet-derived growth factor 2 (SIS
 A;Reference number: A23532; MUID:86205961
 A;Accession: A23532
 A;Molecule type: mRNA
 A;Residues: 1-241 <RAO1>
 A;Cross-references: GB:M12783; GB:M16288; NID:G338210; PIDN:AAA60553.1; PID:G338211
 R;Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober, J.S.
 Nature 316, 748-750, 1985
 A;Title: Cultured human endothelial cells express platelet-derived growth factor B chain
 A;Reference number: A93366; MUID:85296313
 A;Accession: A93366
 A;Molecule type: mRNA
 A;Residues: 1-241 <COL>
 A;Cross-references: GB:X02811; NID:G35371; PIDN:CAA26579.1; PID:G35372
 R;Welch, H.A.; Seidall, W.; Schaiter, H.U.; Hoppe, J.
 FEBS Lett. 198, 344-348, 1986
 A;Title: The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which cod
 A;Reference number: A25141; MUID:86164981
 A;Accession: A25141
 A;Molecule type: mRNA
 A;Residues: 26-241 <WE1>
 A;Cross-references: GB:X03702; NID:G35374; PIDN:CAA27333.1; PID:G35375
 R;Antonlades, H.N.; Hunkapiller, M.W.
 Science 220, 963-965, 1983
 A;Title: Human platelet-derived growth factor (PDGF): amino-terminal amino acid sequence
 A;Reference number: A94271; MUID:83197379
 A;Accession: A94271
 A;Molecule type: protein
 A;Residues: 82-100, 'E', 102-104, 'C', 106, 'C', 108-110 <AMT>
 R;Waterfield, M.D.; Scerace, G.T.; Whittle, N.; Stroobant, P.; Johansson, A.; Wasteson, A.
 Nature 304, 35-39, 1983
 A;Title: Platelet-derived growth factor is structurally related to the putative transfor
 A;Reference number: A93308; MUID:83244981
 A;Accession: A93308
 A;Molecule type: protein
 A;Residues: 82-112 <MAT>
 R;Josephs, S.F.; Guo, C.; Ratner, L.; Wong-Staal, F.
 Science 223, 487-491, 1984
 A;Title: Human proto-oncogene nucleotide sequences corresponding to the transforming reg
 A;Accession: A43499
 A;Reference number: A43499; MUID:84097555
 A;Accession: A43499
 A;Molecule type: DNA

A;Residues: 'Q', 22-241 <JOS2>
 R;Lu, K.V.; Rohde, M.F.; Thomason, A.R.; Kenney, W.C.; Lu, H.S.
 Biochem. J. 309, 411-417, 1995
 A;Title: Mistranslation of a TGA termination codon as tryptophan in recombinant plate
 A;Reference number: S56115; MUID:95351967
 A;Accession: S56115
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 82-93 <LKR>
 R;Rao, C.D.; Pech, M.; Robbins, K.C.; Aaronson, S.A.
 Mol. Cell. Biol. 8, 284-292, 1988
 A;Title: The 5' untranslated sequence of the c-sis/platelet-derived growth factor 2 t
 A;Reference number: 157635; MUID:88094398
 A;Accession: 157635
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-20 <RAO2>
 A;Cross-references: GB:M19719; NID:G189727; PIDN:AAA60349.1; PID:G553608
 R;Ratner, L.; Josephs, S.F.; Jarrett, R.; Reitz, M.S.
 Nucleic Acids Res. 13, 5007-5018, 1985
 A;Title: Nucleotide sequence of transforming human c-sis cDNA clones with homology to
 A;Reference number: 137266; MUID:85269623
 A;Accession: 137266
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-241 <RAO>
 A;Cross-references: EMBL:X02744; NID:G30246; PIDN:CAA26524.1; PID:G30247
 R;Johansson, A.; Heldin, C.H.; Wasteson, A.; Westermark, B.; Deuel, T.F.; Huang, J.S.;
 EMBO J. 3, 921-928, 1984
 A;Title: The c-sis gene encodes a precursor of the B chain of platelet-derived growth
 A;Reference number: A55030; MUID:84236121
 A;Accession: A55030
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 'T', 17-20, 'RQ', 22-241 <JOH>
 A;Cross-references: GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562
 R;Dicks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
 Nucleic Acids Res. 23, 2815-2822, 1995
 A;Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis int
 A;Reference number: S58382; MUID:95388493
 A;Accession: S58383
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 'K', 17-20 <DIR>
 A;Cross-references: EMBL:X83705; NID:G951023; PIDN:CAA58679.1; PID:G951025
 R;Cook, A.L.; Kirwin, P.M.; Craig, S.; Bawden, L.J.; Green, D.R.; Price, M.J.; Richar
 Biochem. J. 281, 57-65, 1992
 A;Title: Purification and analysis of proteinase-resistant mutants of recombinant pla
 A;Reference number: 138108; MUID:92117992
 A;Accession: 138108
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 'W', 82-241 <COO>
 A;Cross-references: EMBL:X65966; NID:G311378; PIDN:CAA5383.1; PID:G35377
 A;Note: mutagenized recombinant sequence
 C;Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal
 C;Genetics:
 A;Gene: GDB:PDGFB
 A;Cross-references: GDB:120709; OMIM:190040
 A;Map position: 22q12.3-22q13.1
 A;Introns: 57/3; 94/1; 192/3; 241/1
 C;Complex: homodimer; heterodimer (see PIR:PFHUG1)
 C;Keywords: growth factor; mitogen
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-81/Domain: amino-terminal propeptide #status predicted <PRO>
 F:82-190/Product: platelet-derived growth factor chain B #status experimental <MAT>
 F:155-163/Region: receptor binding #status predicted
 F:191-241/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:197-141, 130-178, 134-180/Disulfide bonds: #status experimental
 F:124/Disulfide bonds: Interchain (to 133 in homodimeric form) #status experimental
 F:113/Disulfide bonds: Interchain (to 124 in homodimeric form) #status experimental


```

Query Match          10.6%; Score 76; DB 2; Length 452;
Best Local Similarity 21.8%; Pred. No. 8.7;
Matches 22; Conservative 22; Mismatches 33; Indels 24; Gaps 4;

OY 23 VSQDPAHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVQRCGGC 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 LSGKQMGKNERELASFND-----KVROGSYPCS-----TCPMLPVCQGGSC 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 83 PD---DGLECVPTGQHOVRMQLMIRPSSQLGEMSLSEHS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 PKSWLEGEPCPSAKHNIE-ORLLTYALSRIEREANQEA 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 38
T31560
hypothetical protein Y105C5A.c - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T31560
R:McMurray, A.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21045
A:Accession: T31560
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54983.1; CESP:Y105C5A.c
A:Experimental source: clone Y105C5A
C:Genetics:
A:Gene: CESP:Y105C5A.c
A:Introns: 18/73
C:Superfamily: gliadin

Query Match          10.5%; Score 75.5; DB 2; Length 335;
Best Local Similarity 23.7%; Pred. No. 7.4;
Matches 27; Conservative 18; Mismatches 58; Indels 11; Gaps 3;

OY 26 PDAGHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVQRCGG 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 PVAPVQCCPSCMPCEQSCVAPAPVYISLNEVPPCQCCQCAPCQCPSCQCCQN 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 81 CCPDGLCEVPTGQHOVRMQLMIRPSSQLGEMSLSEHSQC--ECRPKKKDSA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TCQ---QYAPVCCQCCQCAPCQCTFSPAPACQCCQCTQCCQCTQCCQCPA 230
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 39
AG0273
probable iron-sulfur protein YP02245 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0273
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2000
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0273
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC91051.1; PID:g15980245; GSPDB:GN00175
C:Genetics:
A:Gene: YP02245
C:Superfamily: conserved hypothetical protein H11684; ferredoxin 2[4Fe-4S] homology

Query Match          10.4%; Score 75; DB 2; Length 188;
Best Local Similarity 27.8%; Pred. No. 4.8;
Matches 25; Conservative 13; Mismatches 40; Indels 12; Gaps 4;

```

```

OY 8 LLAALLAPAAQAPVSPDPAHQKRVSWIDYTRATCQ-----PREVVPLTVELM 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 LKIAELLAVEP--QPLDDESAHQKRVAFIDENICIGTCKICQACVDAITGAT-RAM 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 62 GTVAKOLVPSCTVQRCGGCCPDGLECVP 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 HTVLSDLCTGC---DLCAVAPCPPTDCEIMIP 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 40
T31559
hypothetical protein Y105C5A.b - Caenorhabditis elegans
N:Alternate names: Y105C5A.e
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T31559; T31562
R:McMurray, A.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21045
A:Accession: T31559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54982.1; CESP:Y105C5A.b
A:Experimental source: clone Y105C5A
A:Accession: T31562
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54985.1; CESP:Y105C5A.e
A:Experimental source: clone Y105C5A
C:Genetics:
A:Gene: CESP:Y105C5A.b; CESP:Y105C5A.e
A:Introns: 18/73
C:Superfamily: gliadin

Query Match          10.4%; Score 75; DB 2; Length 335;
Best Local Similarity 24.4%; Pred. No. 8.3;
Matches 30; Conservative 18; Mismatches 51; Indels 24; Gaps 6;

OY 19 AQAAPVS-QPDA-PGHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVQRCGG 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 APAPVQCCPSCMPCEQSCVAPAPVYISLNEVPPCQCCQCAPCQCPSCQCCQN 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 73 -VTVQRCGGCCPDGLECVPPTGQHOVRMQLMIRPSSQLGEMSLSEHSQC--ECRPKK 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 APQCCQCCQNTCQ---QYAPVCCQCCQCTFSPAPACQCCQCTQCCQCTQCCQCPA 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 130 DSA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 QPA 230
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 41
T31840
hypothetical protein T05B4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31840
R:Bradshaw, H.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid T05B4.
A:Reference number: Z21092
A:Accession: T31840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <BRA>
A:Cross-references: EMBL:AF016445; PIDN:AAC69056.1; GSPDB:GN00023; CESP:T05B4.4
A:Experimental source: strain Bristol N2; clone T05B4
C:Genetics:
A:Gene: CESP:T05B4.4
A:Map position: 5

```

C:Accession: T21791
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C:Species: Caenorhabditis elegans
C:myb/nucleic_acid_protein F53E6.10 - Caenorhabditis elegans

R;Gardner, A.
submitted to the EMBL data library, November 1996
A;Reference number: Z19472
A;Accession: T21785
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-249 <will>
A;Cross-references: EMBL:Z81529; PIDN:CAB04291.1; GSPDB:GN00023; CESP:F35E8.10
A;Experimental source: clone F35E8
A;Accession: T21791
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-249 <will>
A;Cross-references: EMBL:Z81529; PIDN:CAB04291.1; GSPDB:GN00023; CESP:F35E8.13
A;Experimental source: clone F35E8
C;Genetics:
A;Gene: CESP:F35E8.10; CESP:F35E8.13
A;Map position: 5
A;Intons: 33/3; 121/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C49G7.3

Query Match 10.1%; Score 72.5; DB 2; Length 249;
Best Local Similarity 27.5%; Pred. No. 11;
Matches 28; Conservative 8; Mismatches 41; Indels 25; Gaps 5;
QY 21 APVSGPDAFGHQRKVSMDVYTRATCOPREVVVPLIYELMGIVAKOLVPSCTVYQRCGG 80
Db 58 APVADGVPSPGRDQGRPLACTATATPAV-----VQDMKMAAQSTCP-----RTGGL 107
QY 81 CCPDGLGCVPTGQHGVNMQILMIRYPSSQLGEMSLSEHSOC 122
Db 108 CCQTSGYNC-PN-----VAIPRLNCGTITA---SOC 134

Search completed: September 10, 2002, 02:51:08
Job time: 3576 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 02:49:22 ; Search time 24.95 seconds
(without alignments)
211.056 Million cell updates/sec

Title: US-09-912-436-6
Perfect score: 719
Sequence: 1 MSPILRLRLAALLQLAPAQ.....EHSQCCECPKPKDSAVKPD 136

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105223

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 99%
Listing first 45 summaries

Database : SwissProt-40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	95.7	207	1	VEGB_BOVIN
2	644	89.6	207	1	VEGB_MOUSE
3	521	72.5	135	1	VEGB_RAT
4	275.5	38.3	190	1	VEGB_HORSE
5	270.5	37.6	190	1	VEGB_PIG
6	269.5	37.5	190	1	VEGB_MESAU
7	269.5	37.5	214	1	VEGB_RAT
8	268.5	37.3	214	1	VEGB_CANFA
9	267.5	37.2	214	1	VEGB_MOUSE
10	266.5	37.1	190	1	VEGB_BOVIN
11	264	36.7	232	1	VEGB_HUMAN
12	263.5	36.6	146	1	VEGB_SHEEP
13	254.5	35.4	164	1	VEGB_CAVPO
14	236	32.8	216	1	VEGB_CHICK
15	199.5	27.7	133	1	VEGB_ORFN2
16	181.5	25.2	149	1	PLGF_BOVIN
17	176.5	24.5	221	1	PLGF_HUMAN
18	176	24.5	158	1	PLGF_RAT
19	176	24.5	158	1	PLGF_MOUSE
20	155.5	21.6	358	1	VEGB_MOUSE
21	149.5	20.8	326	1	VEGB_RAT
22	147	20.4	354	1	VEGB_MOUSE
23	146.5	20.4	354	1	VEGB_MOUSE
24	145.5	20.2	148	1	VEGB_HUMAN
25	145	20.2	419	1	VEGB_MOUSE
26	129	17.9	211	1	PDGF_HUMAN
27	127.5	17.7	213	1	PDGF_HUMAN
28	127	17.7	204	1	PDGF_RAT
29	127	17.7	211	1	PDGF_MOUSE
30	127	17.7	245	1	PDGF_FELCA
31	123	17.1	226	1	PDGF_SMSAV
32	123	17.1	241	1	PDGF_HUMAN
33	119	16.6	226	1	PDGF_XENLA

34	114.5	15.9	225	1	PDGF_RAT	Q05028	rattus norv
35	114	15.9	241	1	PDGF_MOUSE	P31240	mus muscu
36	108	15.0	241	1	PDGF_SHEEP	O95229	ovis aries
37	104.5	14.5	126	1	VEGB_RAT	O35757	rattus norv
38	78	10.8	378	1	DNJ2_MYCLE	O49762	mycobacteri
39	73.5	10.2	1416	1	YNB1_CAEEL	O03610	caenorhabdi
40	72.5	10.1	591	1	GRN_CAVPO	P28797	cavia porce
41	72.5	10.1	1064	1	CY4_RAT	P26770	rattus norv
42	72.5	10.1	1097	1	CCT_DROME	O96433	drosophila
43	71	9.9	356	1	HXB2_HUMAN	P14652	homo sapien
44	71	9.9	751	1	SM3C_MOUSE	O62181	mus muscu
45	70.5	9.8	550	1	YL00_MYCTU	Q10709	mycobacteri

ALIGNMENTS

RESULT 1
VEGB_BOVIN STANDARD: PRT; 207 AA.
AC O9XS49: O9XS48: O9GLX2:
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF).
GN VEGFB OR VRF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Ox NCBI_TaxID=9913;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 38-104 FROM N.A.
RC TISSUE=Heart;
RA Mandriota S.J., Pepper M.S.;
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
CC - FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds heparin and neuropilin-1 whereas the binding to neuropilin-1 of VEGF-B186 is regulated by proteolysis (By similarity).
CC - SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer with vegf (By similarity).
CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC - ALTERNATIVE PRODUCTS: At least 2 isoforms: VEGF-B186 (shown here) and VEGF-B167; are produced by alternative splicing.
CC - PTM: VEGF-B186 is O-glycosylated (By similarity).
CC - SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC EMBL; AB004273; BAAT7686.1; -
CC EMBL; AB004273; BAAT7685.1; -
CC EMBL; AF099134; AAC29746.1; -
CC HSSP: P15692; IVP.
CC InterPro: IPR000072; PDGF.
CC Pfam: PF00341; PDGF; 1.
CC ProDom: PD001629; PDGF; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.

Qy	61	MGYAKOLVPCGVYQRCGGCCPDGGLFCVPTGCGOVMQILMTIRYSPSOLGEMSLERHS	120
Dy	61	MGNVVKOLVPCSVTYQRCGGCCPDGGLFCVPTGCGOVMQILMTIOYPSOGLGEMSLERHS	120
Qy	121	QCECRPKKKDSAVKPD	136
Dy	121	QCECRPKKKESAVKPD	136
Db	121	QCECRPKKKESAVKPD	136
RESULT	3		
VEGB_RAT	STANDARD:	PRT:	135 AA.
AC	035485.054881.		
DT	01-MAR-2002 (Rel. 41, Created)		
DT	01-MAR-2002 (Rel. 41, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Vascular endothelial growth factor B (VEGF-B) (VEGF related factor)		
DE	(VRF) (Fragment).		
GN	VEGFB OR VRF.		
OS	Rattus norvegicus (Rat).		
OC	Eumetazoa; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B186).		
RC	STRAIN=Sprague-Dawley; TISSUE=Placenta;		
RL	Mandriota S.J., Pepper M.S.;		
RL	submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.		
RP	[2]		
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B167).		
RC	TISSUE=Heart;		
RA	Well J., Eschenhagen T., Mittleman C., Scholz H.;		
RL	Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.		
CC	-1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds		
CC	heparin and neuropilin-1 whereas the binding to neuropilin-1 of		
CC	VEGF-B186 is regulated by proteolysis (By similarity).		
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer		
CC	with vegf (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or		
CC	to the extracellular matrix unless released by heparin (By		
CC	similarity).		
CC	-1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)		
CC	and VEGF-B167; are produced by alternative splicing.		
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.		
CC			
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF032925; AAB86884.1; -		
DR	EMBL; AF022952; AAB95447.1; -		
DR	HSSP; P15692; IVP.		
DR	Interpro: IPR000072; PDGF.		
DR	Pfam: PF00341; PDGF_1.		
DR	Prodom: PD001629; PDGF_1.		
DR	SMART; SM00141; PDGF_1.		
DR	PROSITE; PS00249; PDGF_1; 1.		
DR	PROSITE; PS0278; PDGF_2; 1.		
KW	Mitogen; Growth factor; Heparin-binding; Alternative splicing;		
KW	Multigene family.		
FT	NON_TER	1	
FT	DISULFID	47	91
FT	DISULFID	51	93
FT	DISULFID	41	41
FT	DISULFID	50	50
FT	VARSPLIC	106	>135
FT			
FT			
FT	CONFLICT	29	29

FT	CONFLICT	37	37	L -> F (IN REF. 2).
FT	CONFLICT	98	98	R -> K (IN REF. 2).
FT	NON_TER	135	135	
SO	SEQUENCE	135 AA;	15001 MW;	A915863d8586f82d CRC64;
	Query Match	72.5%	Score 521;	DB 1: Length 135;
	Best Local Similarity	89.5%;	Pred. No. 9.3e-47;	
	Matches	94;	Conservative	7; Mismatches 4; Indels 0; Gaps 0;
OY	32	ORKVYSWIDVYTRACQREVVVPLTVELMGVAVALPSCVTVORCGCCPPDDGLECPV	91	
DB	1	KRVVSMWIDVYARATCGREVVVPLSMELMGVAVAKQVLPSCVTVORCGCCPPDDGLECPV	60	
OY	92	TGQHOVMOILMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD	136	
DB	61	IGQHOVMOILMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD	105	
RESULT	4			
ID	VEGA_HORSE	STANDARD;	PRT;	190 AA.
AC	09GKR0:			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).			
DE	VEGF OR VEGFA.			
GN	Equus caballus (Horse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	11			
RP	SEQUENCE FROM N. A.			
RA	Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S.,			
RA	Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;			
RT	"Cloning of cDNA and high-level expression of equine vascular endothelial growth factor (VEGF).";			
RT	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.			
RL	-1- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).			
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with p1GF (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC				
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CC				
DR	EMBL: AB053350: BAB0890.1; -			
DR	InterPro: IPR000072; PDGF.			
DR	Pfam: PF00341; PDGF; 1.			
DR	ProDom: PD001629; PDGF; 1.			
DR	SMART: SM00141; PDGF; 1.			
DR	PROSITE: PS00249; PDGF_1; 1.			
DR	PROSITE: PS00278; PDGF_2; 1.			
KW	Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Multigene family.			
FT	SIGNAL	1	26	POTENTIAL.
FT	CHAIN	27	190	VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT	DISULFID	51	93	BY SIMILARITY.
FT	DISULFID	82	127	BY SIMILARITY.
FT	DISULFID	86	129	BY SIMILARITY.
FT	DISULFID	76	76	INTERCHAIN (BY SIMILARITY).

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF063013; AAK00049.1; -.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
KW Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 190
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
SQ SEQUENCE 190 AA: 22276 MW: F00C5A8EA79A465F CRC64;

Query Match 37.5%; Score 269.5; DB 1; Length 190;
Best Local Similarity 44.3%; Pred. No. 9.3e-21;
Matches 54; Conservative 20; Mismatches 45; Indels 3; Gaps 2;

OY 10 LALLLLPAPAPVSPDPADPAGHQRK--VSMIVYVTRATCPREVVPLVILMGTVAKQ 67
DB 12 LALLLLVHAHAKMSQAPRTTEBQAKHCVFEMVYRKYCHPIETLVLDIQETPDELEYI 71
OY 68 LVPSCVTVORCGCCPDGEGVPCQHOVROMILMR-YPSQLGEMSLSEHSQCRCR 126
DB 72 FKPSCVPLMRGCGCCSDEALECVPTSESNITMQIMRVKPHQSHIGMSFLQHSRCRCR 131
OY 127 KK 128
DB 132 KK 133

RESULT 7
VEGA_RAT STANDARD; PRT; 214 AA.
ID VEGA_RAT
AC P16612; Q9QXG7; Q9QXG6; Q9QXK7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.
RX MEDLINE=90207249; PubMed=2320579;
RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
RA Palist T.M., Hope D.A., Thomas K.A.;
RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT that is homologous to platelet-derived growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-A188; VEGF-A164; VEGF-A144 AND
RP VEGF-A120).
RA Ishii H., Arakawa T., Okayama M., Oota I., Takuma T., Inomata K.;
RT "developmental expression of vascular endothelial growth factor-A
RT (VEGF-A) splicing variants, VEGF-A188, VEGF-A164, and VEGF-A120 in rat
RT mesenter muscle.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]
RP SEQUENCE OF 27-40.
RC TISSUE=Glial tumor;
RX MEDLINE=95221439; PubMed=7706320;
RA Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,
RA Soderman D.D., Palist T.M., Sullivan K.A., Thomas K.A.;
RT "Purification and characterization of a naturally occurring vascular
RT endothelial growth factor:placenta growth factor heterodimer.";
RL J. Biol. Chem. 270:7717-7723(1995).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted.
CC VEGF-A164 is more basic, has heparin-binding properties and,
CC although a significant proportion remains cell-associated, most is
CC freely secreted. VEGF-A188 is very basic; it is cell-associated
CC after secretion and is bound avidly by heparin and the
CC extracellular matrix, although it may be released as a soluble
CC form by heparin, heparinase or plasmin (By similarity).
CC -1- ALTERNATIVE PRODUCTS: At least 4 isoforms: VEGF-A188 (shown here),
CC VEGF-A164, VEGF-A144 and VEGF-A120; are produced by alternative
CC splicing.
CC -1- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in
CC particularly in supraoptic and paraventricular nuclei and the
CC choroid plexus. Also found abundantly in the corpus luteum of
CC the ovary and in kidney glomeruli.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M32167; AAA41211.1; -.
DR EMBL: AF215725; AAF19211.1; -.
DR EMBL: AF215726; AAF19212.1; -.
DR EMBL: AF222779; AAF25958.1; -.
DR PIR: A35987; A35987.
DR HSSP: P15692; IVP.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
KW Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 214
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT VARPPLIC 140 140
FT VARPPLIC 141 164
FT VARPPLIC 141 208
FT VARPPLIC 165 208
FT CONFLICT 101 101
SQ SEQUENCE 214 AA: 25239 MW: 60FBB876F5304946 CRC64;

Query Match 37.5%; Score 269.5; DB 1; Length 214;
Best Local Similarity 43.8%; Pred. No. 1.1e-20;

	Matches	57	Conservative	21;	Mismatches	47;	Indels	5;	Gaps	3
QY	10	LALLQLAPAAQAPVSO	PAGHOR--KVVSWIDVTYRATCQREPVVPLTVELMGTVAKQ	67						
			: : : : :			: : : : :		:		
Dd	12	LALLLLHHAKMSQAAP	PTTEGEOKAHEVVKFMDVYORSYCRLPTELTLDIFOEVPDEIEYI	71						
QY	68	LVPSCVTYORCGGCG	CPDDELCEVPNGOHVNOIMIR-YPSSQLGEMLEHESQCECRP	126						
			: : : : :			: : : : :		: : : : :		
Dd	72	KFPSCPLMKRCAGCN	DEALCECVPTSSESNVMOIKRKPHOSQHIGEMSFLHSRCECRP	131						
QY	127	KKKDSAVKPD	136							
			: :							
Dd	132	KK--DRTKE	139							
			: :							
		VEGF_CANPA								
RESULT	B									
ID	AD	VEGA_CANPA	STANDARD:	PRT:	214	AA.				
DT	01-MAR-2002	(Rel. 41, Created)								
DT	01-MAR-2002	(Rel. 41, Last sequence update)								
DT	01-MAR-2002	(Rel. 41, Last annotation update)								
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).									
GN	VEGF OR VEGFA.									
OC	Canis familiaris (Dog).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.									
OX	NCHI_TaxID=9615;									
RN	[1]	SEQUENCE FROM N.A. (ISOFORM VEGF188).								
RX	MEDLINE=2012516;	PubMed=1061874;								
RA	Scheidegger P., Weidhofer W., Suarez S., Kaser-Holz B., Steiner R., Ballmer-Hofer K., Jauss I. R.									
RT	"Vascular endothelial growth factor (VEGF) and its receptors in tumor-bearing dogs".									
RL	Biol. Chem. 380:1449-1454(1999).									
RN	[2]	SEQUENCE FROM N.A. (ISOFORMS VEGF188; VEGF-182 AND VEGF-164).								
RP	TISSUE=Heart;									
RA	Jingjing L., Roque R.S.;									
RL	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.									
CC	-1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Flt-1 and VEGFR2/Kkr receptors and to heparan sulfate and heparin (By similarity).									
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).									
CC	-1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).									
CC	-1- ALTERNATIVE PRODUCTS: At least 3 isoforms; VEGF188 (shown here), VEGF182 and VEGF164; are produced by alternative splicing.									
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.									
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CC										
DR	EMBL, AJ133758;	CAB82426.1;	-							
DR	EMBL, AF133250;	AAD29684.1;	-							
DR	EMBL, AF133249;	AAD29683.1;	-							
DR	EMBL, AF133248;	AAD29682.1;	-							
DR	InterPro: IPRO00072;	PDGF.								
DR	Pfam: PF00341;	PDGF.	1.							
DR	SMART: PD001629;	PDGF.	1.							
DR	SMART: SM00141;	PDGF.	1.							

DR	PROSITE: PS000249; PGCF_1; 1.
KW	Prosite; PS00278; PGCF_2; 1.
DR	Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KM	Heparin-binding; Alternative splicing; Multigene family.
FT	SIGNAL 1 26
FT	CHAIN 27 214
FT	DISULFID 51 93
FT	DISULFID 82 127
FT	DISULFID 86 129
FT	DISULFID 76 76
FT	DISULFID 85 85
FT	CARBOHYD 100 100
FT	VARSPLIC 140 140
FT	VARSPLIC 141 164
FT	VARSPLIC 159 164
FT	CONFLICT 143 143
FT	CONFLICT 161 161
FT	SEQUENCE 214 AA; 25175 MW; 0AC980A158C44B27 CRC64;
SO	
Query Match	37.3%; Score 268.5; DB 1; Length 214;
Best Local Similarity	45.1%; Pred. No. 1.3e-20;
Matches	55; Conservative 21; Mismatches 43; Indels 3; Gaps 2.
QY	10 LALLQLAPADQAPVSPDAPGHQR--KVVSMDIVYTRATCPREVVVPLVLMGTAKQ 67
DB	12 LLLLLHHAKSSQAAPMAGGEHKPHEVVKFMDVYQSYCRPLETLVDFIOFEYDEIEYI 71
QY	68 LVPSCYVQRCGCCGCPDGLCEVPPGQHQHYRQIILMR-YPSQLGEMSLHSHQCECRP 126
DB	72 FKPSCPMLRCGCGCDEGLCEVPTEEFNITQIMIKIPHQGHGEMSLQHSKCECRP 131
QY	127 KR 128
DB	132 KR 133
RESULT	9
VEGA_MOUSE	
ID	VEGA_MOUSE STANDARD; PRT; 214 AA.
AC	000731;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN	VEGF OR VEGFA.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid	10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORMS VEGF-1, VEGF-2 AND VEGF-3).
RX	MEDLINE=92274860; PubMed=1592003;
RA	Breier G., Albrecht U., Sterrer S., Risau W.;
RT	"Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation.";
RL	Development 114:521-532(1992).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM VEGF-1).
RX	MEDLINE=92355593; PubMed=1644816;
RA	Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT	"Vascular endothelial growth factor. Regulation by cell differentiation and activated second messenger pathways.";
RL	J. Biol. Chem. 267:16317-16322(1992).
RN	[3]
RP	SEQUENCE OF 1-3 FROM N.A.
RX	MEDLINE=96216498; PubMed=8632007;
RA	Shima D.T., Kuroki M., Deutsch U., Ng Y., Adams A.P., D'Amore P.A.;
RT	"The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and characterization of transcriptional and post-transcriptional regulatory sequences.";
RT	

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RL J. Biol. Chem. 271:3877-3883(1996).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (by similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (by similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3
CC remains cell-surface associated unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; VEGF-3/VEGF188 (shown here),
CC VEGF-1/VEGF164 and VEGF-2/VEGF120, are produced by alternative
CC splicing.
CC -1- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the
CC choroid plexus, paraventricular neuroepithelium, placenta and
CC kidney glomeruli. Also found in bronchial epithelium, adrenal
CC gland and in seminiferous tubules of testis. High expression of
CC VEGF continues in kidney glomeruli and choroid plexus in adults.
CC -1- DOMAIN: VEGF-3 contains a basic insert which acts as a cell
CC retention signal.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S37052; AAB2252.1; -
DR EMBL: S38083; AAB2253.1; -
DR EMBL: S38100; AAB2254.1; -
DR EMBL: M95200; AAA0347.1; -
DR EMBL: U41383; -; NOT_ANNOTATED_CDS.
DR PIR: A43351; A43351.
DR HSSP: P15692; 2VPF.
DR MGD: MGI:103178; Vegf.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 1 214
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT VARSPLIC 140 140
FT VARSPLIC 141 164
FT VARSPLIC 141 208
FT CONFLICT 117 118
SQ SEQUENCE 214 AA; 25283 MW; B540B51E4BB6B17 CRC64;

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Query Match 37.2%; Score 267.5; DB 1; Length 214;
Best Local Similarity 42.3%; Pred. No. 1.7e-20;
Matches 55; Conservative 23; Mismatches 47; Indels 5; Gaps 3;

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OY 10 LAALLGLAPAAVQADPAAGHOR--KVYSIMIVYTRATCGPREVYVPLVELMGTYAKQ 67
DB 12 LALLLLHAAKMSQAAPTEEGEOKSHVIRKFMVYRSTCRPLETLDIOETPDEIETI 71
OY 68 LVPSCTVVRGCGCCPDGLEGVPTGQHOVROMIIMIR-YPSQLGEMSLSEHSQCECRP 126
DB 72 FKPSCTVLRMKACGNDALCEVPTSESNTTMOIMIRIKPQSHIGMSFLQHSRCRCR 131

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OY 127 KKKDSAVKPD 136
DB 132 KK--DRTKPE 139
RESULT 10
VEGA_BOVIN STANDARD; PRT; 190 AA.
ID VEGA_BOVIN
AC P15691;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE=90069608; PubMed=2479986;
RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT "Vascular endothelial growth factor: a new member of the platelet-
RT derived growth factor gene family.";
RL Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
RN [3]
RP SEQUENCE OF 27-31.
RX MEDLINE=89286596; PubMed=2735925;
RA Ferrara N., Henzel W.J.;
RT "Pituitary follicular cells secrete a novel heparin-binding growth
RT factor specific for vascular endothelial cells.";
RL Biochem. Biophys. Res. Commun. 161:851-858(1989).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (by similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (by
CC similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are
CC produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL: M32976; AAA30502.1; -
DR EMBL: M31836; AAA30804.1; -
DR EMBL: M33750; AAA30805.1; -
DR PIR: A33255; A33255.
DR PIR: A33787; A33787.
DR PIR: B40080; B40080.
DR HSSP: P15692; 1VGH.

```


RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (Dec-2000) to the EMBL/GenBank/DBJ databases.
RN [14]
RP PEPLININARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE=90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Lemgruber R., Feder J.;
RL "Human vascular permeability factor. Isolation from U937 cells.";
RN J. Biol. Chem. 264:20017-20024(1989).
RN [15]
RP SEQUENCE OF 27-41.
RX MEDLINE=93145946; PubMed=7678805;
RA Fiedlich B.L., Jaeger B., Schellmann C., Weindel K., Wiltling J.,
RA Kochs G., Marne D., Hug H., Welch H.A.;
RL "Synthesis and assembly of functionally active human vascular
RT endothelial growth factor homodimers in insect cells.";
RN Eur. J. Biochem. 211:19-26(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE=97352774; PubMed=9207067;
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RL "Vascular endothelial growth factor: crystal structure and functional
RT mapping of the kinase domain receptor binding site";
RN Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE=98035455; PubMed=9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RL "The crystal structure of vascular endothelial growth factor (VEGF)
RT refined to 1.93-A resolution: multiple copy flexibility and receptor
binding";
RN Structure 5:1325-1338(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE=99119204; PubMed=9922142;
RA Wiseman C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RL "Crystal structure of the complex between VEGF and a receptor-blocking
peptide.";
RN Biochemistry 37:17765-17772(1998).
RN [19]
RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE=97477915; PubMed=9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RL "1H, 13C, and 15N backbone assignment and secondary structure of the
RT receptor-binding domain of vascular endothelial growth factor";
RN Protein Sci. 6:2250-2260(1997).
RN [20]
RP STRUCTURE BY NMR OF 137-215.
RX MEDLINE=98298440; PubMed=9654701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RL "Solution structure of the heparin-binding domain of vascular
RT endothelial growth factor";
RN Structure 6:637-648(1998).
RN [21]
RP FUNCTION.
RX MEDLINE=21320570; PubMed=11427521;
RA Murphy J.F., Fitzgerald D.J.;
RL "Vascular endothelial growth factor induces cyclooxygenase-dependent
RT proliferation of endothelial cells via the VEGF-2 receptor.";
RN FASEB J. 15:1667-1669(2001).
RN [22]
RP FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC -1 SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).

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CC      -1- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
CC      VEGF15 is more basic, has heparin-binding properties and,
CC      although a significant proportion remains cell-associated, most is
CC      freely secreted. VEGF189 is very basic; it is cell-associated
CC      after secretion and is bound avidly by heparin and the
CC      extracellular matrix, although it may be released as a soluble
CC      form by heparin, heparinase or plasmin.
CC      -1- ALTERNATIVE PRODUCTS: 7 isoforms; VEGF206 (shown here), VEGF189,
CC      VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be
CC      produced by alternative splicing.
CC      -1- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms
CC      are widely expressed, whereas the VEGF206 and VEGF-145 are
CC      uncommon.
CC      -1- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,
CC      nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.
CC      -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC      -1- DATABASE: NAME=RED Systems' cytokine mltr-reviews: VEGF;
CC      WWW="http://www.rndsystems.com/asp/g.steibholder.asp?bodyId=230".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC
CC      Query Match          36.7%; Score 264; DB 1; Length 232;
CC      Best Local Similarity 43.9%; Pred. No. 4.2e-20;
CC      Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2
CC
CC      QY      10 LAALLQLAPAPQAPVSPQDPAPG--HQRKVVSIMDYTRATCPREVVVLTVELMGTVAK 66
CC      Db      12 LALLLIHLHNAKSSQAAPMAEFGGQNHNEVKKRMIDYGRSTCHRIETLVIDIPDEYDEIET 71
CC      QY      67 QLVPSCTVYQRCGCGCCRPDDGLECVPTGCHQVHMQLMIR-YSSSOLGEMSLDEHSQCECR 125
CC      Db      72 IKRPSCVPLMRGCGCNDGELCVPTESNITMQIMRIKPHQGNHIGEMSFLOHNCSECR 131
CC      QY      126 PKR 128
CC      Db      132 PKR 134
CC
CC      RESULT 12
CC      VEGA_SHEEP
CC      ID_VEGA_SHEEP STANDARD; PRT; 146 AA.
CC      AC P50412;
CC      DT 01-OCT-1996 (Rel. 34, Created)
CC      DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC      DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC      DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
CC      permeability factor) (VPF).
CC      GN VEGF OR VEGFA.
CC      OS Ovis aries (Sheep).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC      Bovidae; Caprinae; Ovis.
CC      NCBI_TaxID=9940;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RC TISSUE=Kidney;
CC      RX MEDLINE=971117958; Pubmed=8958842;
CC      RA Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
CC      RA Reynolds L.P., Moor R.M.;
CC      RA "Characterization and expression of vascular endothelial growth
CC      RT factor (VEGF) in the ovine corpus luteum.";
CC      RL J. Reprod. Fertl. 108:157-165(1996).
CC      CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC      endothelial cell growth. It induces endothelial cell
CC      proliferation, promotes cell migration, inhibits apoptosis, and
CC      induces permeabilization of blood vessels. It binds to the
CC      VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC      heparin (By similarity).
CC      CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC      with PlGF (By similarity).
CC      CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC      -----

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CC -----
 DR EMBL: X89506; CAA61677.1; -
 DR HSSP: P15692; 1VP.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS0278; PDGF_2; 1.
 DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
 KM Heparin-binding; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 1 26
 FT DISULFID 27 146
 FT DISULFID 51 93
 FT DISULFID 82 127
 FT DISULFID 86 129
 FT DISULFID 76 76
 FT DISULFID 85 85
 FT CARBOHYD 100 100
 SQ SEQUENCE 146 AA; 17247 MW; 4E792CB57F91760 CRC64;

Query Match 36.6%; Score 263.5; DB 1; Length 146;
 Best Local Similarity 44.3%; Pred. No. 3e-20;
 Matches 54; Conservative 23; Mismatches 42; Indels 3; Gaps 2;

OY 10 LALLDLAPADVPDPADGPHOR--KVVSMDVYTRATCPREVVVPLTVELMGTVAKQ 67
 DB 12 LALLDLIHHAKMSQAPPMAGSGKRPHEVMYQSRFPIETLVDIQEYRDELFEFT 71
 OY 63 LVSVCYVORCGCCPDGLEGVPTGQHOVMOILMIR-YPSQJGEMSLSEHSQCECRP 126
 DB 72 FKPSCVPLMRGCGCNDSELCVPTSEFNITQIMRIKPHQSOHIGEMSFLOHNSKCECRP 131

OY 127 KK 128
 DB 132 KK 133

RESULT 13
 VEGA_CAVPO STANDARD: PRT; 164 AA.

ID VEGA_CAVPO STANDARD: PRT; 164 AA.
 AC P26617;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
 factor) (VPF).
 GN VEGF OR VEGFA.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blle duct;
 RA Berse B.;
 RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Growth factor active in angiogenesis, and endothelial
 CC cell growth. Induces endothelial proliferation and vascular
 CC permeability (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with p1GF (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin (By
 CC similarity).

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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CC -----
 DR EMBL: M84230; AAA37057.1; -
 DR HSSP: P15692; 1VGH.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS0278; PDGF_2; 1.
 DR Mitogen: Angiogenesis; Growth factor; Glycoprotein.
 KM Heparin-binding; Multigene family.
 FT SIGNAL 25 67
 FT CHAIN 25 67
 FT DISULFID 56 101
 FT DISULFID 60 103
 FT DISULFID 50 50
 FT DISULFID 59 59
 FT CARBOHYD 74 74
 SQ SEQUENCE 164 AA; 19330 MW; 9EB86A19AD5DCA4 CRC64;

Query Match 35.4%; Score 254.5; DB 1; Length 164;
 Best Local Similarity 45.8%; Pred. No. 2.8e-19;
 Matches 49; Conservative 20; Mismatches 35; Indels 3; Gaps 2;

OY 26 PDAPGHQ--RKVVSMDVYTRATCPREVVVPLTVELMGTVAKQLYPSCVTVORCGCCP 83
 DB 2 PMAGSGKRPHEVMYQSRFPIETLVDIQEYRDELFEFTYFAPSCVPLMRGCGCN 61
 OY 84 DDLGECVPTGQHOVMOILMIR-YPSQJGEMSLSEHSQCECRPKK 129
 DB 62 DESLSECVPTSEFNITQIMRIKPHQSOHIGEMSFLOHNSKCECRPKE 108

RESULT 14
 VEGA_CHICK STANDARD: PRT; 216 AA.

ID VEGA_CHICK STANDARD: PRT; 216 AA.
 AC P52582; O91420;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS *Gallus gallus* (Chicken), and
 OS *Coturnix coturnix japonica* (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Heart;
 RA Takahashi T.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC [2]
 CC SEQUENCE FROM N.A.
 CC SPECIES=C. japonica; TISSUE=Embryo;
 CC MEDLINE=96005007; PubMed=7556923;
 CC Flamme I., von Reutern M., Drexler H.C., Syed-Ali S., Risau W.;
 CC "Overexpression of vascular endothelial growth factor in the avian
 CC embryo induces hypervascularization and increased vascular
 CC permeability without alterations of embryonic pattern formation.";
 CC Dev. Biol. 171:399-414(1995).
 CC [3]

RP SEQUENCE OF 60-187 FROM N.A.
RC SPECIES=C.C.JAPONICA;
RX MEDLINE=95301109; PubMed=7781909;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT differentiation in the quail embryo.";
RL Dev. Biol. 169:699-712(1995).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Elt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms: VEGF190 (shown here),
CC VEGF166 and VEGF146; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Abundantly and equally expressed in heart and
CC liver. In kidney glomeruli, brain and yolk sac, VEGF166 is 5- to
CC 10-times more abundant than VEGF190.
CC -1- DEVELOPMENTAL STAGE: VEGF166 is expressed early at day 1 and is
CC upregulated during gastrulation. Expression of VEGF190 is detectable
CC only from day 2.
CC -1- DOMAIN: VEGF190 contains a basic insert which acts as a cell
CC retention signal.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC -----
DR EMBL: AB011078; BAA24925.1; -
DR EMBL: S79680; AAB35371.1; -
DR HSSP: P15692; 1VGH.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT CHAIN 1 26
FT SIGNAL 1 26
FT CHAIN 27 216
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77
FT DISULFID 86 86
FT CARBOHYD 101 101
FT VARSPLIC 142 142
FT VARSPLIC 143 166
FT VARSPLIC 166 166
FT VARSPLIC 167 210
SQ SEQUENCE 216 AA; 25203 MW; 82E669C2F6C6DA7 CRC64;
Query Match 32.8%; Score 236; DB 1; Length 216;
Best Local Similarity 40.7%; Pred. No. 3e-17;
Matches 50; Conservative 21; Mismatches 48; Indels 4; Gaps 2;

QY 126 PKR 128
Db 132 PKR 134
RESULT 15
VEGH_ORFN2
ID VEGH_ORFN2 STANDARD; PRT; 133 AA.
AC P52584;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vascular endothelial growth factor homolog precursor.
GN A2R.
OS Orf virus (strain NZ2) (OV NZ-2).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OX NCBI_TaxID=10259;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94076465; PubMed=8254780; S.B., Mercer A.A., Robinson A.J.;
RA Lytle D.J., Fraser K.M., Fleming S.B.,
RT "Homologs of vascular endothelial growth factor are encoded by the
RT poxvirus orf virus.";
RL J. Virol. 68:84-92(1994).
CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC -----
DR EMBL: S67520; AAB29220.2; -
DR HSSP: P15692; 1VPP.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Mitogen: Growth factor; Glycoprotein; Signal.
KW CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 133
FT DISULFID 36 78
FT DISULFID 67 112
FT DISULFID 71 114
FT DISULFID 61 61
FT DISULFID 70 70
FT CARBOHYD 85 85
SQ SEQUENCE 133 AA; 14715 MW; 917C0F6883030C39 CRC64;
Query Match 27.7%; Score 199.5; DB 1; Length 133;
Best Local Similarity 39.6%; Pred. No. 1e-13;
Matches 36; Conservative 19; Mismatches 35; Indels 1; Gaps 1;

QY 38 MIDYTRATCPREVVPVPLVELMGVAKQLVPSCTVORCGCCPDGECVPTGQHOV 97
Db 27 WSEVLKSGSECKPRPIVVPVSETHPELTSORENPPCVILMRGCGCCNDSELCVPTBEVNV 86
QY 98 RMQILMIRYPSO-IIGKMSLEHSQCCRPK 127
Db 87 SMELLGASGSGSGNGMORLSFVEHKKCDCKPR 117
RESULT 16

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PLGF_BOVIN
ID PLGF_BOVIN STANDARD: PRT: 149 AA.
AC Q9XS47;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Placenta growth factor precursor (PLGF).
GN PGF OR PLGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family."
RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
CC -! FUNCTION: Growth factor active in angiogenesis, and endothelial
CC cell growth, stimulating their proliferation and migration. It
CC binds to receptor VEGFR-1/Flt1 (By similarity).
CC -! SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
CC heterodimer with VEGF/VEGF-A (By similarity).
CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
CC -! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC -----
DR EMBL: AB004272; BAA77684.1; -
DR HSSP: P15692; 1VPE.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
KM Mitogen; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 149
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77
FT DISULFID 86 86
FT CARBOHYD 33 33
FT CARBOHYD 101 101
SEQUENCE 149 AA: 17094 MW: 18883BC745FEED CRC64;

Query Match 25.2%; Score 181.5; DB 1; Length 149;
Best Local Similarity 32.2%; Pred. No. 8, 1e-12;
Matches 39; Conservative 21; Mismatches 60; Indels 1; Gaps 1;

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RESULT 17
ID PLGF_HUMAN STANDARD: PRT: 221 AA.
AC P49763; Q9BV78; Q9Y6S8; Q07101;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Placenta growth factor precursor (PLGF).
GN PGF OR PLGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
RC TISSUE=Placenta;
RA Maglione D., Guerriero V., Vigiiletto G., Dell-I-Bovi P., Persico M.G.;
RT "Isolation of a human placenta cDNA coding for a protein related to
RT the vascular permeability factor."
RL Proc. Natl. Acad. Sci. U.S.A. 88:9267-9271(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
RC TISSUE=Placenta;
RA Hauser S.D., Welch H.A.;
RT "A heparin-binding form of placenta growth factor (PLGF-2) is
RT expressed in human umbilical vein endothelial cells and in
RT placenta."
RL Growth Factors 9:259-268(1993).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM PLGF-2).
RA Maglione D., Guerriero V., Vigiiletto G., Ferraro M.G., Aprelikova O.,
RA Alfaiolo K., del Vecchio S., Lei K.-J., Chou J.Y., Persico M.G.;
RT "Two alternative mRNAs coding for the angiogenic factor, placenta
RT growth factor (PLGF), are transcribed from a single gene of
RT chromosome 14."
RL Oncogene 8:925-931(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-3).
RC TISSUE=Placenta;
RA Maglione D., Guerriero V., Vigiiletto G., Ferraro M.G., Aprelikova O.,
RA Cao Y., Ji W.-R., Qi P., Rosin A., Cao Y.;
RT "Placenta growth factor: identification and characterization of a
RT novel isoform generated by RNA alternative splicing."
RL Biochem. Biophys. Res. Commun. 235:493-498(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Dickhoff R., James R.,
RA Loretz C., Lasky S., Madan A., Prescott S., Ratcliffe A., Shaffer T.,
RA Hood L.;
RT "Sequencing of human chromosome 14."
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
RC TISSUE=Muscle, and Placenta;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
RN [7]
RP CHARACTERIZATION, AND SEQUENCE OF 19-24.
RA MEDLINE=95014370; PubMed=7929268;
RA Park J.E., Chen H.H., Winer J., Houck K.A., Ferrara N.;
RT "Placenta growth factor. Potential of vascular endothelial growth
RT factor bioactivity, in vitro and in vivo, and high affinity binding
RT to Flt-1 but not to Flt-1/KDR."
RL J. Biol. Chem. 269:25646-25654(1994).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) (ISOFORM PLGF-1).
RA MEDLINE=21192270; PubMed=11069911;
RA Iyer S., Leonidas D.D., Swaminathan G.J., Maglione D., Battisti M.,
RA Tucci M., Persico M.G., Acharya K.R.;
RT "The crystal structure of human placenta growth factor-1 (PLGF-1), an

```


CC	vessels. May function in the formation of the venous and lymphatic
CC	vascular systems during embryogenesis, and also in the maintenance
CC	of differentiated lymphatic endothelium in adults. Binds and
CC	activates VEGFR-3 (Flt4) receptor.
CC	-1-SUBUNIT: Homodimer; non-covalent and antiparallel.
CC	-1-SUBCELLULAR LOCATION: Secreted.
CC	-1-TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC	-1-DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC	body structures and organs of the embryo such as limb buds,
CC	acoustic ganglion, teeth, heart, anterior pituitary as well as
CC	lung and kidney mesenchyme, liver, derma, and perosteum of the
CC	vertebral column.
CC	-1-INDUCTION: By the transcription factor c-fos.
CC	-1-FTM: Undergoes a complex proteolytic maturation which generates a
CC	variety of processed secreted forms with increased activity toward
CC	VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC	linked by disulfide bonds before secretion. The fully processed
CC	VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC	bound by non-covalent interactions (By similarity).
CC	-1-SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X99572: CAA67892.1; -
DR	EMBL; D89628: BAA14002.1; -
DR	HSSP; P15692: IVP.
DR	MGD; MGI:108037; Fltgf.
DR	InterPro; IPRO00072: PDGF.
DR	Pfam; PF00341: PDGF_1.
DR	ProDom; PD001629: PDGF_1.
DR	SMART: SM00141; PDGF_1.
DR	PROSITE; PS00249; PDGF_1; 1.
DR	PROSITE; PS50278; PDGF_2; 1.
KW	Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
RK	Cleavage on pair of basic residues; Multigene family.
FT	SIGNAL
FT	PROPEP
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	DISULFD
FT	DISULFD
FT	DISULFD
FT	DISULFD
FT	DISULFD
FT	CARBOHYD
FT	CARBOHYD
SO	SEQUENCE
Query Match	Best local similarity
Matches	Conservative
34 KVVSMIDYTRATCPREVNVPLVTFLMGAKQVLVPSGVTVQRGGCCPDGLBCVPTG	Score 155.5; DB 1; Length 358;
11: : : : : : : : : : : : : : :	33.3%; Pred. No. 9.2e-09;
105 KYID--EEMQRFQSGPREVCVEVASLELGKTNTTFPKPCPVNVRFGCGCNEGVMCMNTS	Matches 32; Conservative 16; Mismatches 43; Indels 5; Gaps 2;
94 QHQVKMQLMTIRPSSQJGEM---SLEHSQCCEPR	126
: : : : : : : : : : : : : : : : : : : : : : : : :	
163 TSYISKOLFETSVPLTSVDLPVRIANTGTCKAP	198

RESULT	21			
VEGD_RAT		STANDARD:	PRT:	326 AA.
ID	VEGD_RAT			
AC	035251;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (Ftgr).			
DE	Ftgr OR VEGF-D.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RA	Yamada Y., Hirata Y., Nezu J., Shimane M.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).			
CC	-1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	-1- PM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	-----			
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CC	-----			
DR	EMBL; AF014827; AAB66557.1; -			
DR	HSSP; P15692; 1VP.			
DR	InterPro: IPR000072; PDGF.			
DR	Pfam; PF00341; PDGF_1.			
DR	ProDom; PD001629; PDGF; 1.			
DR	SMART; SM00141; PDGF_1.			
DR	PROSITE; PS00249; PDGF_1; 1.			
DR	PROSITE; PS0278; PDGF_2; 1.			
KW	Mitogen: Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.			
FT	SIGNAL	1	21	POTENTIAL.
FT	PROPEP	22	93	POTENTIAL.
FT	CHAIN	94	210	VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT	PROPEP	211	326	POTENTIAL.
FT	DOMAIN	227	317	4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1..3)-C.
FT				1 (APPROXIMATE).
FT	REPEAT	227	242	
FT	REPEAT	263	278	
FT	REPEAT	282	298	
FT	REPEAT	306	317	3.
FT	DISULFID	116	158	4 (INCOMPLETE).
FT	DISULFID	147	194	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	151	196	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	141	141	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	150	150	INTERCHAIN (BY SIMILARITY).
FT	CARBOHD	160	160	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	190	190	N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 37112 MM; 1261AFA373596C00 CRC64;

Query Match 20.8%; Score 149.5; DB 1; Length 326;
Best Local Similarity 32.3%; Pred. No. 3.5e-08;
Matches 31; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

OY 34 KVSIVDYVTRATCOPREVVVPLVFLMGTAKOLVPSGVYQRCGCCPDGECVPTG 93
DB 105 KVID--EEMQRQCSPRETCVAVASELGTNTTFKPCVAVNFRGCCNESHVCMNTS 162

OY 94 QHVRMOILMIRYPSQJGEM---SLEHSGCECRP 126
DB 163 TSYSKOLFELISVPLTSVPELVPVKIANHGCCKLP 198

RESULT 22
VEGC_MOUSE STANDARD; PRT; 415 AA.

AC P97953;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-l).
DE VEGFC.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=97164697; PubMed=9012504;
RA Kukk E., Lymbousaki A., Taira S., Kaipainen A., Jeltsch M., Jounk V., Allitalo K.;
RT "VEGF-C receptor binding and pattern of expression with VEGFR-3 suggests a role in lymphatic vascular development.";
RL Development 122:3829-3837(1996).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 108-126.
RC STRAIN-BALB/C;
RX MEDLINE=97388482; PubMed=9247316;
RA Flitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R., Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciavatta A., Giannotti J., Finerly H., Zollner R., Beler D.R., Leak L.V., Turner K.J., Wood C.R.;
RT "Characterization of murine Flt4 ligand/VEGF-C";
RL Oncogene 15:613-618(1997).
CC -1- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in angiogenesis of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expression detected in mesenchymal cells of postimplantation embryos, particularly in the regions where the lymphatic vessels undergo sprouting from embryonic veins, such as the perimetonephric, axillary and jugular regions, and in the developing mesenterium. Expressed in adult heart, brain, spleen, lung, liver, skeletal muscle and kidney.
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3, but only the fully processed form could activate VEGFR-2. VEGF-C first form an antiparallel homodimer linked by disulfide bonds. Before secretion, a cleavage occurs between arg-227 and ser-228 producing an heterotetramer. The next extracellular step of the processing removes the N-terminal propeptide. Finally the

CC mature VEGF-C is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC -----

DR EMBL; U73620; AAC52984.1; -;
DR EMBL; U58112; AAB46707.1; -;
DR HSSP; P15692; 1VPF.
DR MGD; MGI:109124; Vegfc.
DR InterPro; IPR004153; CXXC.
DR InterPro; IPR002400; GF_cysknob.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF03128; CXXC; 5.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GRCYSKNOF.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0276; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
FT SIGNAL 1 31
FT PROPEP 32 107
FT CHAIN 108 223
FT PROPEP 224 415
FT DOMAIN 276 358
FT FT 276 291
FT REPEAT 300 315
FT REPEAT 324 339
FT REPEAT 343 358
FT DISULFID 127 169
FT DISULFID 158 205
FT DISULFID 162 207
FT DISULFID 152 152
FT DISULFID 161 161
FT CARBOHYD 171 171
FT CARBOHYD 201 201
FT CARBOHYD 236 236
SQ SEQUENCE 415 AA; 46471 MM; D9D3DD3CECC659D6 CRC64;

Query Match 20.4%; Score 147; DB 1; Length 415;
Best Local Similarity 32.7%; Pred. No. 8e-08;
Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

OY 28 APGHQKVSIVDYVTRATCOPREVVVPLVFLMGTAKOLVPSGVYQRCGCCPDG 86
DB 107 AAHNTETLKSIDEMKRTQCPREVCIDVKGEGGAATNTFFKPCVAVNFRGCCNSEG 166

OY 87 LECVPTGQHVRMOILMIRYPSQJGEM---MSLEHSGCECRP 127
DB 167 LQCMNTSTGYLSKTLFELTVPLSGRPKVTISFANHNSCRM 210

RESULT 23
VEGC_HUMAN STANDARD; PRT; 354 AA.

AC O43915;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FlGF).
GN FIGF OR VEGFD.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=97349118; PubMed=9205122;
 RX Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
 RT "Molecular cloning of a novel vascular endothelial growth factor,
 VEGF-D.";
 RL Genomics 42:483-488(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=98140120; PubMed=9479493;
 RX Rocchiccioli M., Lestini M., Luddi A., Orlandini M., Franco B.,
 RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
 RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
 between the PIGA and the GRPR genes.";
 RL Genomics 47:207-216(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98118549; PubMed=9435229;
 RA Achen M.G., Jeltsch M., Kuk E., Maekinen T., Vitall A., Wilks A.F.,
 RA Allitalo K., Stacker S.A.;
 RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
 tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4)."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
 RN [4]
 RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
 RX MEDLINE=20011413; PubMed=10542248;
 RA Stacker S.A., Stenvers K.L., Caesar C., Vitall A., Domagala T.,
 RA Nice E.C., Routhal S., Simpson R.J., Moritz R., Karpanen T.,
 RA Allitalo K., Achen M.G.;
 RT "Biosynthesis of vascular endothelial growth factor-D involves
 proteolytic processing which generates non-covalent homodimers.";
 RL J. Biol. Chem. 274:32127-32136(1999).
 CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
 and endothelial cell growth, stimulating their proliferation and
 migration and also has effects on the permeability of blood
 vessels. May function in the formation of the venous and lymphatic
 vascular systems during embryogenesis, and also in the maintenance
 of differentiated lymphatic endothelium in adults. Binds and
 activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
 CC -1- SUBUNIT: Homodimer, non-covalent and antiparallel.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
 intestine and fetal lung, and at lower levels in skeletal muscle,
 colon, and pancreas.
 CC -1- PTM: Undergoes a complex proteolytic maturation which generates a
 variety of processed secreted forms with increased activity toward
 VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
 linked by disulfide bonds before secretion. The fully processed
 VEGF-D is composed mostly of two VEGF homology domains (VHDS)
 bound by non-covalent interactions.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D89630; BAA24264.1; -;
 DR EMBL: Y12863; CAA73370.1; -;
 DR EMBL: Y12864; CAA73371.1; -;
 DR EMBL: Y12865; CAA73371.1; JOINED.
 DR EMBL: Y12866; CAA73371.1; JOINED.
 DR EMBL: Y12867; CAA73371.1; JOINED.
 DR EMBL: Y12868; CAA73371.1; JOINED.
 DR EMBL: Y12869; CAA73371.1; JOINED.

DR EMBL: Y12870; CAA73371.1; JOINED.
 DR EMBL: AJ000185; CAA03942.1; -;
 DR MTM: 300091; -;
 DR HSSP: P15692; 1VPP.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF_1.
 DR ProDom: PD001629; PDGF_1.
 DR SMART: SM00141; PDGF_1.
 DR PROSITE: PS00249; PDGF_1.
 DR PROSITE: PS00278; PDGF_2; 1.
 DR MitoGen: growth factor; Glycoprotein; Signal; Repeat;
 KW cleavage on pair of basic residues; Multigene family.
 FT SIGNAL 1 21
 FT PROPEP 22 88
 FT CHAIN 89 205
 FT PROPEP 206 354
 FT DOMAIN 222 318
 FT REPEAT 222 237
 FT REPEAT 258 273
 FT REPEAT 277 293
 FT REPEAT 301 318
 FT DISULFID 111 153
 FT DISULFID 142 189
 FT DISULFID 146 191
 FT DISULFID 136 136
 FT DISULFID 145 145
 FT CARBOHYD 155 155
 FT CARBOHYD 185 185
 FT CARBOHYD 287 287
 SQ SEQUENCE 354 AA; 40444 MW; 204BD769D735173E CRC64;
 Query Match 20.4%; Score 146.5; DB 1; Length 354;
 Best Local Similarity 32.3%; Pred. No. 7.7e-08;
 Matches 31; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

OY 34 KYVSMIDVYRATRCQREVVYPLVELMGVAVKQVSCYTVYORGGCCDDGLECYPTG 93
 DB 100 IVID--EEMORTCSPRETEVEVASELKGSTNFFKPCVNVFRCGCCNEESLGMTS 157
 OY 94 OHQVMOILMIRYPSOLGEM---SLEHSQCECRP 126
 DB 158 TSYISKPLFETISVPLTISVPELVKPVKANHGCCLP 193
 RESULT 24
 VEGH ORFN7 STANDARD; PRT; 148 AA.
 AC P52585;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vascular endothelial growth factor homolog precursor.
 GN A2R.
 OS Orf virus (strain NZ7) (OV NZ-7).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Parapoxvirus.
 OX NCBI_TaxID=73495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94076465; PubMed=8254780;
 RA Lytle D.J., Frazer K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
 RT "Homologs of vascular endothelial growth factor are encoded by the
 J. Virol. 68:84-92(1994)."
 RL J. Virol. 68:84-92(1994).
 CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; S67522; AAB29223.1; -.
DR	HSSP; P15692; 2VPE.
DR	InterPro; IPR000072; PDGF.
DR	Pfam; PF00341; PDGF_1.
DR	ProDom; PD001629; PDGF; 1.
DR	SMART; SM00141; PDGF_1.
DR	PROSITE; PS00249; PDGF_1; FALSE.NEG.
DR	PROSITE; PS50278; PDGF_2; 1.
KW	Mitogen; Growth factor; Glycoprotein; Signal.
FT	SIGNAL
FT	1 25
FT	POTENTIAL.
FT	26 148
FT	CHAIN
FT	
FT	
FT	DISULFID
FT	46 88
FT	BY SIMILARITY.
FT	DISULFID
FT	77 130
FT	BY SIMILARITY.
FT	DISULFID
FT	81 132
FT	BY SIMILARITY.
FT	DISULFID
FT	71 71
FT	INTERCHAIN (BY SIMILARITY).
FT	DISULFID
FT	80 80
FT	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD
FT	95 95
FT	N-LINKED (GLCNAC...) (POTENTIAL).
SO	SEQUENCE
	148 AA; 16078 MW; FEI13BA104CCT3F8 CRC64; 2

Query Match	20.28	Score	145.5	DB	1	Length	148
Best Local Similarity	30.58	Pred. No.	4e-08				
Matches	39	Conservative	23	Mismatches	53	Indels	13
						Gaps	4

```

QY      7  RLILAAALLQLRLPAAPARPSOP--DAGHQRKVVSMYIDVTALACQREVVVPLTVELAMSTVA 65
      8  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      8  QVVALLITCMNLNPECVASQSNDSPPSTN--DMWRITLDSCKCRPRDVPVYLAGEEYPESTN 64

QY      66  KQIVPCSTTVYORCGCGCGDDGLGC--PTGQHQVORMQIMIRY-----SGLGEMSL 116
      67  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65  LQYNRCVATYAKRSCGCGMGDQDICTAVETRNFTVYSYTGVSSESGTNGSVINLQRIYV 124

QY      117  EHSQCEC 124
      118  : : : : :
Db      125  TEHTKDCD 132

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RESULT	25
VEGC_HUMAN	VEGC_HUMAN
ID	VEGC_HUMAN
STANDARD:	PRT;
419	AA.
AC	P49767;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4-ligand) (Flt4-l).
GN	VEGFC.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI	TaxID:9606;
OX	[1]
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RP	MEDLINE=96178224; PubMed=8617204;
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinnen N., Alltalo K.;
RT	"A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.",
RL	EMBO J. 15:290-298(1996).
RL	[2]
RP	ERRATUM.
RX	MEDLINE=96203094; PubMed=8612600;
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinnen N., Alltalo K.;
RA	EMBO J. 15:1751-1751(1996).
RL	[3]

RP SEQUENCE FROM N.A.
RC TISSUE-Glial tumor; PubMed=6700872;
RX MEDLINE=96312526;
RA Lee J., Gray A., Yuan Y., Luo S.-M., Avraham H., Wood W.I.;
RT "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1998-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97388482; PubMed=9247316;
RA Fitz L.J., Morris J.C., Towler P., Long A., Burgess J., Greco R.,
RA Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarietta A.,
RA Giannotti J., Flinnerty H., Zollner R., Beier D.R., Leak L.V.,
RA Turner K.J., Wood C.R.;
RT "Characterization of murine Flt4 ligand/VEGF-C";
RL Oncogene 15:613-618(1997).
RN [5]
RP SEQUENCE OF 32-41; 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227.
RX MEDLINE=97377029; PubMed=9233800;
RA Joukov V., Sorsa T., Kumar V., Jeleitch M., Cleason-Welsh L., Cao Y.,
RA Saksela O., Kalkkinnen N., Allalao K.;
RT "Proteolytic processing regulates receptor specificity and activity of
RT VEGF-C";
RL EMBL J. 16:3898-3911(1997).
CC -I- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC cell growth, stimulating their proliferation and migration and
CC also has effects on the permeability of blood vessels. May
CC function in angiogenesis of the venous and lymphatic vascular
CC systems during embryogenesis, and also in the maintenance of
CC differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -I- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Spleen, lymph node, thymus, appendix, bone
CC marrow, heart, placenta, ovary, skeletal muscle, prostate, testis,
CC colon and small intestine and fetal liver, lung and kidney, but
CC not in peripheral blood lymphocyte.
CC -I- PFM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC VEGF-C first form an antiparallel homodimer linked by disulfide
CC bonds. Before secretion, a cleavage occurs between arg-227 and
CC ser-228 producing a heterotetramer. The next extracellular step
CC of the processing removes the N-terminal propeptide. Finally the
CC mature VEGF-C is composed mostly of two VEGF homology domains
CC (VHDS) bound by non-covalent interactions.
CC -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X94216; CAA63907.1; -
DR EMBL; U43142; AAA85214.1; -
DR EMBL; U58111; AAB02909.1; -
DR HSSP; P15692; IYFP.
DR MIM; 601528; -
DR InterPro; IPR004153; CXKCXC.
DR InterPro; IPR002400; GF_cyskn0t.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF03128; CXKCXC; 5.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKN0T.
DR PRODOM; PR0001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PSS0278; PDGF_2; 1.
DR MitoGen; Growth factor; Glycoprotein; Signal; Repeat;
RW Cleavage on pair of basic residues; Multigene family.

DR EMBL: X99216; CAA63907.1; -.
DR EMBL: U04342; AAA85214.1; -.
DR EMBL: U58111; AAB02909.1; -.
DR HSSP: P15692; 1VPF.
DR MIM: 601528; -.
DR InterPro: IPR004153; CXXCXC.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF03128; CXXCXC; 5.
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR Mitogen: Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.

FT SIGNAL 1 31
 FT PROPEP 32 111
 FT CHAIN 112 227
 FT PROPEP 228 419
 FT DOMAIN 280 362
 FT REPEAT 280 295
 FT REPEAT 304 319
 FT REPEAT 328 343
 FT REPEAT 347 362
 FT DISULFID 131 173
 FT DISULFID 162 209
 FT DISULFID 166 211
 FT DISULFID 156 156
 FT DISULFID 165 165
 FT CARBOHYD 175 175
 FT CARBOHYD 205 205
 FT CARBOHYD 240 240
 FT MUTAGEN 227 227
 SO SEQUENCE 419 AA; 46883 MM; 9F598719DB3E014F CRC64;
 Query Match 20.2%; Score 145; DB 1; Length 419;
 Best Local Similarity 32.7%; Pred. No. 1.3e-07;
 Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;
 OY 28 APGHQRKRVSWIDYTRAT-CQPREVVVPLTVELMGTVAKQVPSCTVORCGCCPDG 86
 DB 111 AAHYNEILKSDINEMKRTQCMPEVCIDVGEFGVATNTFFKPCVSVYRCGCGCNSG 170
 OY 87 LECPTGQHVQRMQILMIRPSSQLGE---MSLEHSGCCRPK 127
 DB 171 LQCKNTSTSLTKTEITVPLSGPKPVITSEANHTSCRMK 214
 RESULT 26
 PDGA_HUMAN STANDARD; PRT; 211 AA.
 AC P04085;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 DE (PDGF-1).
 GN PDGFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144463; PubMed=3422746;
 RA Bonthron D.T., Morton C.C., Orkin S.H., Collins T.;
 RT "Platelet-derived growth factor A chain: gene structure, chromosomal
 location, and basis for alternative mRNA splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1492-1496(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144698; PubMed=2832727;
 RA Rorsman F., Bywater M., Knott T.J., Scott J., Betsholtz C.;
 RT "Structural characterization of the human platelet-derived growth
 factor A-chain cDNA and gene: alternative exon usage predicts two
 RT different precursor proteins."
 RL Mol. Cell. Biol. 8:571-577(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86203630; PubMed=3754619;
 RA Betsholtz C., Johansson A., Heldin C.H., Westermark B., Lind P.,
 RA Ureda M.S., Eddy R., Shown T.B., Philpott K., Mellor A.L., Knott T.J.,
 RA Scott J.;
 RT "cDNA sequence and chromosomal localization of human platelet-derived
 RT growth factor A-chain and its expression in tumour cell lines";

RL Nature 320:695-699(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88030061; PubMed=3666150;
 RA Hoppe J., Schumacher U., Eichner W., Weich H.A.;
 RT "The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only
 RT distantly related."
 RL FEBS Lett. 223:243-246(1987).
 RN [5]
 RP SEQUENCE OF 1-53 FROM N.A.
 RX MEDLINE=93252628; PubMed=8486521;
 RA Takimoto Y., Li W.Y., Wang Z.Y., Tong B.D., Deuel T.F.;
 RT "Nucleotide sequence of the 5' region of the human platelet-derived
 RT growth factor A-chain gene."
 RL Hiroshima J. Med. Sci. 42:47-52(1993).
 RN [6]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=87287247; PubMed=3614363;
 RA Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Rices G., McConathy E.,
 RA Drohan W., Deuel T.F.;
 RT "cDNA clones reveal differences between human glial and endothelial
 RT cell platelet-derived growth factor A-chains."
 RL Nature 328:619-621(1987).
 RN [7]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=87287248; PubMed=3614364;
 RA Collins T., Bonthron D.T., Orkin S.H.;
 RT "Alternative RNA splicing affects function of encoded platelet-derived
 RT growth factor A chain."
 RL Nature 328:621-624(1987).
 RN [8]
 RP INTERCHAIN DISULFIDE BONDS.
 RX MEDLINE=92283833; PubMed=1317862;
 RA Andersson M., Oestman A., Baeckstroem G., Hellman U.,
 RA George-Nascimento C., Westermark B., Heldin C.-H.;
 RT "Assignment of interchain disulfide bonds in platelet-derived growth
 RT factor (PDGF) and evidence for agonist activity of monomeric PDGF."
 RL J. Biol. Chem. 267:11260-11266(1992).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
 CC retention signal.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -1- DATABASE: NAME-R&D systems' cytokine minireviews: PDGF;
 CC WWW="http://www.rndsystems.com/asp/g/sitebuilder.asp?bodyid=220".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M21571; -; NOT_ANNOTATED_CDS.
 DR EMBL; X03795; CAA27421.1; -;
 DR EMBL; X06374; CAA29677.1; -;
 DR EMBL; M20494; AAA60045.1; -;
 DR EMBL; M20488; AAA60045.1; JOINED.
 DR EMBL; M20489; AAA60045.1; JOINED.
 DR EMBL; M20490; AAA60045.1; JOINED.
 DR EMBL; M20491; AAA60045.1; JOINED.
 DR EMBL; M20492; AAA60045.1; JOINED.

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DR EMBL: M20493; AAA60045.1; JOINED.
DR EMBL: M19988; AAA60046.1; JOINED.
DR EMBL: M21571; AAA60046.1; JOINED.
DR EMBL: M19984; AAA60046.1; JOINED.
DR EMBL: M19985; AAA60046.1; JOINED.
DR EMBL: M19986; AAA60046.1; JOINED.
DR EMBL: M19987; AAA60046.1; JOINED.
DR EMBL: M19989; AAA60047.1; JOINED.
DR EMBL: M21571; AAA60047.1; JOINED.
DR EMBL: M19984; AAA60047.1; JOINED.
DR EMBL: M19985; AAA60047.1; JOINED.
DR EMBL: M19986; AAA60047.1; JOINED.
DR EMBL: M19987; AAA60047.1; JOINED.
DR EMBL: A09204; CAA00830.1; JOINED.
DR EMBL: S62078; AAB26566.1; JOINED.
DR PIR: A28964; PFHUG1.
DR HSP: B28964; B28964.
DR MIM: 173430; 1PDS.
DR InterPro: IPR002400; GF_cysknot.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCSKNOT.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR GlycoProtein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT PROPEP 1 20
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 123 123
FT CARBOHYD 134 132
FT VARSPPLIC 194 196
FT VARSPPLIC 197 211
FT CONFLICT 64 66
SQ SEQUENCE 211 AA; 24043 MW; 48633DE558EFA43 CRC64;

Query Match 17.9%; Score 129; DB 1; Length 211;
Best Local Similarity 28.8%; Pred. No. 2.9e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 28; Gaps 6;

QY 45 ATCCPREVV-VPLTVELMGTVAKOLV-PSCTVYVRCGCGCCPDGLEGVPTGQHQRMOI 101
DB 94 AVCKRTVYIEIPRS-QVDPSTANFLIWPCEVVKRCCTCCNTSSVKQCPSRVHNRHVAV 152

QY 102 LMIRY-----PSSQLGMSLEHSSQEC-----RP-----KKKDSAVKP 135
DB 153 AKVEYVKKPKLKEVQVRLEHLKCACTSLNPDYREEDTGRPRSGKKRRKKRKLKP 210

RESULT 27
PDGA_RABIT STANDARD: PRT; 213 AA.
AC P34007;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
DE (PDGF-1).
GN PDGFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=92246970; PubMed=1575749;
RA Nakahara K.-I., Nishimura H., Kuro-O M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Nagai R.;
RT "Identification of three types of PDGF-A chain gene transcripts in
RT rabbit vascular smooth muscle and their regulated expression during
RT development and by angiotensin II."
RL Blochem. Biophys. Res. Commun. 184:811-818(1992).
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOGENSIN II.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VBGF FAMILY OF GROWTH FACTORS.
DR PIR: J50735; J50735.
DR PIR: PS0387; PS0387.
DR PIR: JN0248; JN0248.
DR HSP: P01127; 1PDG.
DR InterPro: IPR002400; GF_cysknot.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCSKNOT.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT PROPEP 1 20
FT CHAIN 90 213
FT SITE 158 162
FT DISULFID 131 179
FT DISULFID 135 181
FT DISULFID 125 125
FT CARBOHYD 134 134
FT VARSPPLIC 196 198
FT VARSPPLIC 197 213
SQ SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

Query Match 17.7%; Score 127.5; DB 1; Length 213;
Best Local Similarity 30.1%; Pred. No. 4.1e-06;
Matches 34; Conservative 24; Mismatches 46; Indels 9; Gaps 5;

QY 19 AOAIVSOPAPRGHOKRKYVSMIDVTRATQPREVV-VPLTVELMGTVAKOLV-PSCTV 75
DB 71 ARHVAEKPRAPVPVRKRKT-IEAIPALCKRTVYIEIPRS-QVDPSTANFLIWPCEV 128

QY 76 QRCGCGCCPDGLEGVPTGQHQRMOILMIRY-----PSSQLGMSLEHSSQEC 124
DB 129 KRCCTGCCNTSSVKQCPSRVHNRHVAVAKVEYVKKPKLKEVQVRLEHLKCA 181

RESULT 28
PDGA_RAT STANDARD: PRT; 204 AA.
AC P28576;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

```

DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 DE (PDGF-1).
 GN PDGFA OR RPAL.
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE OF 8-204 FROM N.A.
 RX MEDLINE-93305723; PubMed-8318539;
 RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
 RT "Conservation in sequence and affinity of human and rodent PDGF
 RT ligands and receptors.";
 RL Biochim. Biophys. Acta 1173:294-302(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93191115; PubMed-8447423;
 RA Katayose D., Ohe M., Yamauchi K., Ogata M., Shirato K., Fujita H.,
 RA Shibahara S., Takishima T.;
 RT "Increased expression of PDGF A- and B-chain genes in rat lungs with
 RT hypoxic pulmonary hypertension.";
 RL Am. J. Physiol. 264:L100-L106(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RA Xia Y., Feng L., Tang W.W., Wilson C.B.;
 RT "Cloning and expression of rat platelet-derived growth factor
 RT A-chain";
 RL J. Am. Soc. Nephrol. 3:622-622(1992).
 RN [4]
 RP SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).
 RC STRAIN-FISCHER 344; Tissue-Smooth muscle;
 RX MEDLINE-93225589; PubMed-8469035;
 RA Szabo P., Weksler D., Whittington E., Weksler B.B.;
 RT "The age-dependent proliferation of rat aortic smooth muscle cells is
 RT independent of differential splicing of PDGF A-chain mRNA.";
 RL Mech. Ageing Dev. 67:79-89(1993).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a
 CC short form: are produced by alternative splicing.
 CC -1- DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER
 CC BECOMES MORE PREVALENT DURING AGING.
 CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
 CC retention signal.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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 CC -----
 DR EMBL: L06884; AAB59683.1; -
 DR EMBL: Z14120; CAAY8480.1; -
 DR EMBL: D10106; BAA00987.1; -
 DR EMBL: L06238; AAA41932.1; -
 DR EMBL: S57864; AAB26134.2; -
 DR HSSP: P01127; 1PDS.
 DR InterPro: IPR002400; GF-cysknot.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF.1.
 DR PRINTS: PR00438; GFCYSKNOT.

DR Prodom: PD001629; PDGF: 1.
 DR SMART: SM00141; PDGF: 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS0278; PDGF_2; 1.
 KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
 KW signal.
 FT SIGNAL 1 20
 FT PROPEP 21 85 BY SIMILARITY.
 FT CHAIN 86 204 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
 FT SITE 158 162 RECEPTOR BINDING SITE (POTENTIAL).
 FT DISULFID 96 140 BY SIMILARITY.
 FT DISULFID 129 177 BY SIMILARITY.
 FT DISULFID 133 179 BY SIMILARITY.
 FT DISULFID 123 123 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 132 132 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT VARSPLIC 194 196 GRR -> DVR (IN SHORT ISOFORM).
 FT VARSPLIC 197 204 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 85 111 KRISBEAIPAVCKRTVYEIRSOVD -> REVLKRPPO
 FT CONFLICT FARPGRSFTRYGARMT (IN REF. 2).
 FT CONFLICT I -> T (IN REF. 3).
 FT SEQUENCE 119 119
 SQ SEQUENCE 204 AA; 23307 MW; FA413F74E86F742C CRC64;
 Query Match 17.7%; Score 127; DB 1; Length 204;
 Best Local Similarity 31.3%; Pred. No. 4.5e-06;
 Matches 31; Conservativity 20; Mismatches 36; Indels 12; Gaps 5;
 QY 45 ANCPREVV-VPLVETLMGVAKOLV-PSCVTVORCGCCPDGLEGVPTGHOVMOI 101
 DB 94 AACKRTVYIEIPRS-QVDPSTANFLIMPPCVCKRCGTCGNCSTSVKCPBVRHRSVAV 152
 QY 102 LMRV----PSSDLGMSLEFHSQCRCRKKDSAYKP 136
 DB 153 AKVEYRKKRKLKEVQVRLEHLEAC---ATSNLNP 187
 RESULT 29
 PGCA_MOUSE STANDARD; PRT; 211 AA.
 AC P20033;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 DE (PDGF-1).
 GN PDGFA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
 RC STRAIN-BALB/C;
 RX MEDLINE-94031105; PubMed-1340209;
 RA Roisman F., Betscholtz C.;
 RT "Characterization of the mouse PDGF A-chain gene. Evolutionary
 RT conservation of gene structure, nucleotide sequence and alternative
 RT splicing.";
 RL Growth Factors 6:303-313(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC STRAIN-F9;
 RX MEDLINE-90169294; PubMed-2155144;
 RA Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L.,
 RA Stiles C., Bowen-Pope D.;
 RT "Selective expression of PDGF A and its receptor during early mouse
 RT embryogenesis.";
 RL Dev. Biol. 138:114-122(1990).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEALS THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a
CC short form; are produced by alternative splicing.
CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
CC retention signal.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: S66873; AAB28740.2; -
DR EMBL: S66868; AAB28740.2; JOINED.
DR EMBL: S66869; AAB28740.2; JOINED.
DR EMBL: S66870; AAB28740.2; JOINED.
DR EMBL: S66871; AAB28740.2; JOINED.
DR EMBL: S66872; AAB28740.2; JOINED.
DR EMBL: S66874; AAB28741.2; -
DR EMBL: S66868; AAB28741.2; JOINED.
DR EMBL: S66869; AAB28741.2; JOINED.
DR EMBL: S66870; AAB28741.2; JOINED.
DR EMBL: S66871; AAB28741.2; JOINED.
DR EMBL: S66872; AAB28741.2; JOINED.
DR EMBL: M29464; AAA39903.1; -
DR PIR: A37359; A37359.1; -
DR HSSP: P01127; 1PDG.
DR MGD: MGT:97527; PDGfa.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 123 123
FT DISULFID 132 123
FT CARBOHYD 134 134
FT VARSPLIC 194 196
FT VARSPLIC 197 211
FT CONFLICT 92 92
FT CONFLICT 174 174
SQ SEQUENCE 211 AA: 24102 MW: 24102 MW: AC4345A10ECF4B59 CRC64;

Query Match 17.7%; Score 127; DB 1; Length 211;
Best Local Similarity 31.3%; Pred. No. 4.6e-06;
Matches 31; Conservative 20; Mismatches 36; Indels 12; Gaps 5;

DB 153 AKVEYRKPKKEVQVRLBEEHCAC---ATSNLMPD 187
RESULT 30
ID PDGB_FELCA STANDARD; PRT; 245 AA.
AC P12919;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Platelet-derived growth factor, B chain precursor (PDGF B-chain)
DE (PDGB) (c-sis) (PDGF-2).
GN PDGB OR SIS.
OS Fels silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87146463; PubMed=3822831;
RA van den Ouweland A.M.W., van Groningen J.J.M., Schaiken J.A.,
RA van Neck H.W., Bloemers H.P.J., van de Ven W.J.M.;
RT "Genetic organization of the c-sis transcription unit."; Nucleic Acids Res. 15:959-970(1987).
RN [2]
RP REVISIONS.
RA van den Ouweland A.M.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X05112; CAA28758.1; ALT_SEQ.
DR PIR: A26402; TVCTSS.
DR HSSP: P01127; 1PDG.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal.
FT SIGNAL 1 20
FT PROPEP 21 81
FT CHAIN 82 194
FT PROPEP 82 194
FT DISULFID 101 145
FT DISULFID 134 182
FT DISULFID 138 182
FT DISULFID 128 128
FT DISULFID 137 137
SQ SEQUENCE 245 AA: 27787 MW: E7715291D9837512 CRC64;

Query Match 17.7%; Score 127; DB 1; Length 245;

[illegible]

AC P01127:P78431;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Platelet-derived growth factor, B chain precursor (PDGF B-chain)
DE (PDGF-2) (c-sis) (becaplermin).
CN PDGFB OR SIS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=84250225; PubMed=6740330;
RA Josephs S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S.,
RA Wong-Staal F. ;
RT "Transforming potential of human c-sis nucleotide sequences encoding
RT platelet-derived growth factor." ;
RL Science 225:636-639(1984).
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=86205961; PubMed=3517869;
RX Rao C.D., Igarashi H., Chiu I.-M., Robbins K.C., Aaronson S.A. ;
RA "Structure and sequence of the human c-sis/platelet-derived growth
RT factor 2 (Sis/PDGF2) transcriptional unit." ;
RL Proc. Natl. Acad. Sci. U.S.A. 83:2392-2396(1986).
RN [3]
RP SEQUENCE OF 22-241 FROM N.A.
RP MEDLINE=84205633; PubMed=6327048;
RX Chiu I.-M., Reddy E.P., Givol D., Robbins K.C., Tronick S.R.,
RA Aaronson S.A. ;
RT "Nucleotide sequence analysis identifies the human c-sis
RT proto-oncogene as a structural gene for platelet-derived growth
RT factor." ;
RL Cell 37:123-129(1984).
RN [4]
RP SEQUENCE FROM N.A.
RP MEDLINE=85296313; PubMed=4033772;
RX Collins T., Ginsburg D., Boss J.M., Orkin S.H., Pober J.S. ;
RA "Cultured human endothelial cells express platelet-derived growth
RT factor B chain: cDNA cloning and structural analysis." ;
RL Nature 316:748-750(1985).
RN [5]
RP SEQUENCE FROM N.A.
RP MEDLINE=85269623; PubMed=2991848;
RX Rather L., Josephs S.F., Jarrett R., Reitz M.S., Wong-Staal F. ;
RA "Nucleotide sequence of transforming human c-sis cDNA clones with
RT homology to platelet-derived growth factor." ;
RL Nucleic Acids Res. 13:5007-5018(1985).
RN [6]
RP SEQUENCE FROM N.A.
RP MEDLINE=87217119; PubMed=3472769;
RX Rao C.D., Igarashi H., Pech M.W., Robbins K.C., Aaronson S.A. ;
RA "Oncogenic potential of the human platelet-derived growth factor
RT transcriptional unit." ;
RL Cold Spring Harb. Symp. Quant. Biol. 51:959-966(1986).
RN [7]
RP SEQUENCE FROM N.A.
RP Burgess J., Odell C. ;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 1-53 FROM N.A.
RP MEDLINE=97141927; PubMed=8988177;
RX Simon M.-P., Pedoutier F., Sivert N., Mandahl N., Craver R.D.,
RA Colindre J.-M., Terrier-Lacombe M.-J., Mandahl N., Craver R.D.,
RA Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D.,
RA Franssón I., Guilbaud C., Dumanski J.P. ;
RT "Regulation of the platelet-derived growth factor B-chain gene via
RT fusion with collagen gene COL1A1 in dermatofibrosarcoma protuberans
RT and giant-cell fibroblastoma." ;
RL Nat. Genet. 15:95-98(1997).
RN [9]
RP SEQUENCE OF 26-241 FROM N.A.

RA MEDLINE=86164981; PubMed=3456904;
RX Welch H.A., Seibald W., Schairer H.U., Hoppe J.;
RT "The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase
RL mRNA which codes for the sequence of the PDGF-B chain.";

RN [10]
RP SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=84236121; PubMed=6329745;
RA Johnson A., Heldin C.H., Westesson A., Westermark B., Deuel T.F.,
RA Huang J.S., Seeburg P.H., Gray A., Ulrich A., Scrcie G.,
RA Stroobant P., Waterfield M.D.;
RT "The c-sis gene encodes a precursor of the B chain of
RT platelet-derived growth factor.";
RL EMBO J. 3:921-928(1984).
RN [11]
RP SEQUENCE OF 82-110.
RX MEDLINE=83197379; PubMed=6844921;
RA Antoniadou H.N., Hunziker M.W.;
RT "Human platelet-derived growth factor (PDGF): amino-terminal amino
RT acid sequence.";
RL Science 220:963-965(1983).
RN [12]
RP SEQUENCE OF 82-112.
RX MEDLINE=83244981; PubMed=6306471;
RA Waterfield M.D., Scrcie G.T., Whittle N., Stroobant P., Johnson A.,
RA Wasteson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F.;
RT "Platelet-derived growth factor is structurally related to the
RT putative transforming protein p28ts of simian sarcoma virus.";
RL Nature 304:35-39(1983).
RN [13]
RP MUTAGENESIS, AND IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR
RP BINDING.
RX MEDLINE=92097530; PubMed=1661670;
RA Clements J.M., Bowden L.J., Bloxidge R.E., Catlin G., Cook A.L.,
RA Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,
RA Hellewell P.G., Kiaray P.M., Nayes P.D., Richardson S.J., Brown D.,
RA Chawla S.B., Sklar M., Winslow D.;
RT "Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate
RT receptor binding and activation.";
RL EMBO J. 10:4113-4120(1991).
RN [14]
RP INTERCHAIN DISULFIDE BONDS.
RX MEDLINE=92283833; PubMed=1317862;
RA Anderson M., Oestman A., Backstrom G., Hellman U.,
RA George-Nascimento C., Westermark B., Heldin C.H.;
RT "Assignment of interchain disulfide bonds in platelet-derived growth
RT factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
RL J. Biol. Chem. 267:11260-11266(1992).

RN [15]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=93010987; PubMed=1396586;
RA Oefner C., D'Arcy A., Winkler F.K., Eggmann B., Hosang M.;
RL "Crystal structure of human platelet-derived growth factor BB.";

-1 FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS APPARENT RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

-1 SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.

-1 PHARMACEUTICAL: Available under the name Reggrenex (Ortho-McNeil).

-1 used to promote healing in diabetic neuropathic foot ulcers.

-1 MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.

-1 SIMILARITY: BELONGS TO THE PDGFR/VEGF FAMILY OF GROWTH FACTORS.

-1 DATABASE: NAME=R&D Systems' cytokine source book: PDGF;

-1 WWW="http://www.rndsystems.com/aspp/4/sitebuilder.asp?bodyid=220".

-1 DATABASE: NAME=Reggrenex; NOTE=Clinical information on Reggrenex; WWW="http://www.reggrenex.com/".

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CC CC      EMBL; K01401; AAA60552.1; -.
CC CC      EMBL; K01918; AAA60552.1; JOINED.
CC CC      DR EMBL; J00121; AAA60552.1; JOINED.
CC CC      DR EMBL; K01398; AAA60552.1; JOINED.
CC CC      DR EMBL; K01399; AAA60552.1; JOINED.
CC CC      DR EMBL; K01400; AAA60552.1; JOINED.
CC CC      DR EMBL; X02811; CAA26579.1; -.
CC CC      DR EMBL; M12783; AAA60553.1; -.
CC CC      DR EMBL; X02744; CAA26524.1; -.
CC CC      DR EMBL; K01917; AAA98793.1; -.
CC CC      DR EMBL; K01913; AAA98793.1; JOINED.
CC CC      DR EMBL; K01914; AAA98793.1; JOINED.
CC CC      DR EMBL; K01915; AAA98793.1; JOINED.
CC CC      DR EMBL; K01916; AAA98793.1; JOINED.
CC CC      DR EMBL; X03702; CAA27333.1; -.
CC CC      DR EMBL; Z81010; CAB26535.1; -.
CC CC      DR EMBL; X00561; CAA25228.1; -.
CC CC      DR EMBL; X00561; CAA25229.1; -.
CC CC      DR EMBL; X98706; CAA67262.1; -.
CC CC      DR PIR; A94276; PFHUG2.
CC CC      DR PD3; 1PDG; 31-JUN-94.
CC CC      MM; 190040; -.
CC CC      DR InterPro; IPR002400; GF_cysknot.
CC CC      DR InterPro; IPR000072; PDGF.
CC CC      DR Pfam; PF00341; PDGF_1.
CC CC      DR PRINTS; PR00438; GF_CYSKNOT.
CC CC      DR ProDom; PD001629; PDGF_1.
CC CC      DR SMART; SM00141; PDGF_1.
CC CC      DR PROSITE; PS00249; PDGF_1; 1.
CC CC      DR PROSITE; PS50278; PDGF_2; 1.
CC CC      KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal;
CC CC      KW Pharmaceutical; 3D-structure.
CC CC      FT SIGNAL 1 20
CC CC      FT PROPEP 21 81
CC CC      FT CHAIN 82 190 PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
CC CC      FT PROPEP 191 241 INVOLVED IN RECEPTOR BINDING.
CC CC      FT SITE 108 108 INVOLVED IN RECEPTOR BINDING.
CC CC      FT SITE 111 111
CC CC      FT DISULFID 97 141
CC CC      FT DISULFID 130 178 INTERCHAIN.
CC CC      FT DISULFID 134 180 INTERCHAIN.
CC CC      FT DISULFID 124 124
CC CC      FT DISULFID 133 133
CC CC      FT CONFLICT 21 21 E -> R (IN REF. 3).
CC CC      FT CONFLICT 101 101 T -> E (IN REF. 11).
CC CC      FT CONFLICT 105 105 E -> C (IN REF. 11).
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Query Match          17.1%; Score 123; DB 1; Length 241;
Best Local Similarity 34.8%; Pred. No. 1,4e+05;
Matches 31; Conservative 17; Mismatches 29; Indels 12; Gaps 4;
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OY 45 ATCPREVVVDIWEVLWG-TVAKDLV-PSCVTVOAGCGCCPDGGIECVPTGOHOVMQIL 102
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Db 95 AECKTTEVEFFISRLIDRTNANFLVMPVCVEVGRCSCCNRNVQCRRPT---GVQLRPV 151
OY 103 MIR-----YPSOGLGEMSLSEHSOCRC 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 152 QVRKIETVRKKPIFRKATVTLEDHLACKC 180
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RESULT 33
PDGA_XENIA STANDARD; PRT; 226 AA.
AC P13696;
CT 01-JAN-1990 (Rel. 13, Created)
CT 01-JAN-1990 (Rel. 13, Last sequence update)
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DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 DE (PDGFA).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RA MEDLINE=88321676; PubMed-3413486;
 RA Mercola M., Melton D.A., Stiles C.D.;
 RT "Platelet-derived growth factor A chain is maternally encoded in
 RT Xenopus embryos".
 RL Science 241:1223-1225(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=90175018; PubMed-2308861;
 RA Bejcek B.E., Li D.Y., Deuel T.F.;
 RT "Nucleotide sequence of a cDNA clone of Xenopus platelet-derived
 RT growth factor A-chain".
 RL Nucleic Acids Res. 18:680-680(1990).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
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 CC TRANSFORMATION PROCESSES.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, a long form (shown here) and a
 CC short form, are produced by alternative splicing.
 CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
 CC retention signal.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M23237; AAA49927.1; -
 DR EMBL: M23238; AAA49928.1; -
 DR EMBL: X17545; CAA35583.1; -
 DR PIR: S08220; S08220.
 DR HSSP: P01127; 1PDG.
 DR InterPro: IPR002400; GF_cysknoc.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF_1.
 DR PRINTS: PR00438; GFCSKNOT.
 DR PRODom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 KM Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
 KW Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 91
 FT CHAIN 92 226
 FT DISULFID 101 145
 FT DISULFID 134 182
 FT DISULFID 138 184
 FT DISULFID 128 137
 FT DISULFID 137 139
 FT CARBOHYD 139 200
 FT VARSPLIC 138 200
 GFF -> DVR (IN SHORT ISOFORM).

FT VARSPLIC 201 226 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 199 209 MISSING (IN REF. 2).
 FT CONFLICT 218 218 O -> R (IN REF. 2).
 SQ SEQUENCE 226 AA; 25719 MW; E3E724FC67C2FB2 CRC64;
 Query Match 16.6%; Score 119; DB 1; Length 226;
 Best Local Similarity 32.2%; Pred. No. 3.3e-05;
 Matches 28; Conservative 18; Mismatches 33; Indels 8; Gaps 4;
 QY 45 ATGCPREV--VPLTVELMGTVAKOLV-PSCTVYORCGCCPDGLGCVPTGQHYVMQI 101
 DB 99 AICKRTVYIYEIPRS-QIDPTSANPLTPCVCYKRCGTGCMSSVKCGSRRIHRSVKV 157
 QY 102 LMIKY----PSSQLGEMSLPEHSQCEC 124
 DB 158 AKVEYVKKRKIKELVLRLEHLECTC 184
 RESULT 34
 PDGB_RAT STANDARD; PRT; 225 AA.
 AC 005028;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet-derived growth factor, B chain precursor (PDGF B-chain)
 DE (PDGF-2) (Fragment).
 GN PDGB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93305723; PubMed-8318539;
 RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
 RT "Conservation in sequence and affinity of human and rodent PDGF
 RT ligands and receptors".
 RL Biochim. Biophys. Acta 1173:294-302(1993).
 RN [2]
 RP SEQUENCE OF 74-182 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Smooth muscle;
 RX MEDLINE=95277908; PubMed-7758166;
 RA Lindner V., Glachelli C.M., Schwartz S.M., Reidy M.A.;
 RT "A subpopulation of smooth muscle cells in injured rat arteries
 RT expresses platelet-derived growth factor-B chain mRNA".
 RL Circ. Res. 76:951-957(1995).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC MAY HAVE A CHEMOTACTIC ROLE IN INTIMAL THICKENING.
 CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A DISTINCT SUBPOPULATION
 CC OF SMOOTH MUSCLE CELLS IN INJURED ARTERIES.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 CC -----
 DR EMBL: Z14117; CAA78487.1; -
 DR EMBL: LA0991; AAA70048.1; -

ID DNJ2.MYCLE STANDARD: PRT: 378 AA.
AC 049762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chapterone protein dnaj2.
GN DNaj2 OR ML0625 OR B1937_F2_56.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Rodison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,
CC THE ATPASE ACTIVITY OF DNK (BY SIMILARITY).
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNaj FAMILY.
CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC -----
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CC -----
DR EMBL: 000016; AAA17167.1; -;
DR EMBL: AL583919; CAC30133.1; -;
DR HSP: P25685; 1HDJ.
DR LepToma; ML0625; -;
DR InterPro: IPR003095; Dnaj.
DR InterPro: IPR002939; Dnaj_C.
DR InterPro: IPR001305; Dnaj_CXXCXXG.
DR InterPro: IPR001623; Dnaj_N.
DR Pfam: PF00226; Dnaj; 1.
DR Pfam: PF01556; Dnaj_C; 1.
DR Pfam: PF00684; Dnaj_CXXCXXG; 1.
DR PRINTS: PR00625; DnajPROTEIN.
DR SMART: SM00271; Dnaj; 1.
DR PROSITE: PS00636; Dnaj_1; FALSE_NEG.
DR PROSITE: PS0076; Dnaj_2; 1.
DR PROSITE: PS00637; Dnaj_CXXCXXG; FALSE_NEG.
DR Chapterone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KW Complete proteome.
FT DOMAIN 4 68 J-DOMAIN.
FT DOMAIN 80 111 GLY-RICH.
FT REPEAT 141 148 CXXCXXG MOTIF.
FT REPEAT 158 165 CXXCXXG MOTIF.
FT REPEAT 184 191 CXXCXXG MOTIF.
FT REPEAT 198 205 CXXCXXG MOTIF.
FT METAL 141 141 ZINC 1 (BY SIMILARITY).
FT METAL 144 144 ZINC 1 (BY SIMILARITY).
FT METAL 158 158 ZINC 2 (BY SIMILARITY).

FT METAL 161 161 ZINC 2 (BY SIMILARITY).
FT METAL 184 184 ZINC 2 (BY SIMILARITY).
FT METAL 187 187 ZINC 2 (BY SIMILARITY).
FT METAL 198 198 ZINC 1 (BY SIMILARITY).
FT METAL 201 201 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 378 AA: 40399 MW: 723DD8BF6FC62153 CRC64;
Query Match 10.8%; Score 78; DB 1; Length 378;
Best Local Similarity 23.3%; Pred. No. 0.9;
Matches 30; Conservative 18; Mismatches 49; Indels 32; Gaps 4;
QY 29 PGHQRKVSMDVYTRATCPREVV-----PLTVLMLG-----T 63
DB 110 PGSDSLPMMWLDIECATYGTQVYDFAVLCDRCOGKGTNGSDAPICPCGGRGVOT 169
QY 64 VAROLVPCVTVORCGC-----CPDDGLECYPTGHOVROMOILMIRYPSOLGEMSL 117
DB 170 VQSLGQWYVATPCPPCRGVGVYIPDCCGCVGDGRVARRREI-YKIPISGVGDGRVR 228
QY 118 EHSQCECRP 126
DB 229 LAAQGEVGP 237
RESULT 39
ID YN81.CAEEL STANDARD: PRT: 1416 AA.
AC 003610;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 316.1 kDa protein ZC84.1 in chromosome III.
GN ZC84.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Spoat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RC STRAIN-BRISTOL N2;
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO D104.3.
CC -1- SIMILARITY: CONTAINS 5 BPT1/KUNITZ INHIBITOR DOMAINS.
CC -----
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CC -----
DR EMBL: Z19157; CAA79569.1; -;

DR PIR: S28291; S28291.
DR HSSP: P00974; 1BRB.
DR WormPep: ZC84.1; CE15020.
DR InterPro: IPR002899; EB.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002223; Kunitz-BPTI.
DR Pfam: PF01683; EB; 3.
DR Pfam: PF00014; Kunitz-BPTI; 5.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 5.
DR SMART: SM00289; WRL; 13.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 5.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
KW Hypothetical protein; Serine protease inhibitor; Repeat.
FT DOMAIN 212 266 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 337 387 BPTI/KUNITZ INHIBITOR 2.
FT DOMAIN 434 484 BPTI/KUNITZ INHIBITOR 3.
FT DOMAIN 538 590 BPTI/KUNITZ INHIBITOR 4.
FT DOMAIN 646 698 BPTI/KUNITZ INHIBITOR 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CACE1CB22E70D CRC64;

Query Match Best Local Similarity 10.2%; Score 73.5; DB 1; Length 1416;
Matches 40; Conservative 21; Mismatches 39; Indels 69; Gaps 12;

QY 18 PAQAPVSQDPAP-----GHQ-----RKVSWIDYVTRATQCPREVVPFLVELMG 62
DB 1037 PEKCVQGSNCPRGFCACOKSLAGHVCCTVRKV-----ACESNEVITE-----G 1080
QY 63 TVAKQIVP--SCVTVQRC--GCGCPDGLGCVPT-----GQHQVRA--QILM--IRY 106
DB 1081 ECHAQVPGSECLANECTGGSCVEDAKCECRPLKAVGFGCEIQCSSNQVLAHNGLCH 1140
QY 107 PSSOLGEMSL-----EHS-----QCECR-----PKKKDSAV 133
DB 1141 NKAATGEMCLTVRQCENSGCIEGSCCKKFKIEKACKMPEVKKSAV 1189

RESULT 40
GRN_CAVPO STANDARD; PRT; 591 AA.
ID GRN_CAVPO
AC P28797;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 2;
DE Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
DE (Fragment).
GN GRN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
RC TISSUE-Testis;
RX MBLDLINE=93228994; PubMed=8471244;
RA Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Aral Y.,
RA Gerton G.L.;
RT "Acrogranin, an acrosomal cysteine-rich glycoprotein, is the
RT precursor of the growth-modulating peptides, granulins, and
RT epithelins, and is expressed in somatic as well as male germ cells."
RL Mol. Reprod. Dev. 34:233-243(1993).
CC -1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC
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CC -----
DR EMBL: M86735; AAA37030.1; .
DR InterPro: IPR000118; Granulin.
DR Pfam: PF00396; granulin; 7.
DR SMART: SM00277; GRAN; 6.
DR PROSITE: PS00799; GRANULINS; 6.
KW Cytokine; Repeat; signal; Glycoprotein.
FT NON_TER 1 3
FT SIGNAL 1 3
FT CHAIN 4 591 ACGROGRANIN.
FT PEPTIDE 753 798 GRANULIN 1.
FT PEPTIDE 711 764 GRANULIN 2.
FT PEPTIDE 206 261 GRANULIN 3.
FT PEPTIDE 281 335 GRANULIN 4.
FT PEPTIDE 737 745 GRANULIN 5.
FT PEPTIDE 439 494 GRANULIN 6.
FT PEPTIDE 751 769 GRANULIN 7.
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 591 AA; 62586 MW; BE7C9FC8F21CB8A1 CRC64;

Query Match Best Local Similarity 10.1%; Score 72.5; DB 1; Length 591;
Matches 31; Conservative 17; Mismatches 51; Indels 41; Gaps 6;

QY 8 LLLAALLDAPAO-----APVSQDPAGHQKRVSWIDYVTRATQCPREVVPFLT 57
DB 338 LLQVPMQKTRQAPSRSPGPRGPRPPPLRSISQDEV---VSCRGNL----- 389
QY 58 VELMGTVAKQIVPSCVTVQRCGCGCP--DDGLECVPTGQHYVMQILMTRPS-----SQL 111
DB 390 -----CCRLASGEMGCCPSSEGLYCMAGERCQVDRILAPKMAHLMSLSQT 436
QY 112 GEMSLSEHSQC-----ECRPK 127
DB 437 TDVGDQDHASCPVQTCCKP 456

RESULT 41
CYMA_RAT STANDARD; PRT; 1064 AA.
ID CYMA_RAT
AC P26770;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Adenylate cyclase, type IV (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Adenyllyl cyclase).
GN ADCY4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=92052234; PubMed=1946437;
RA Gao B., Gilman A.G.;
RT "Cloning and expression of a widely distributed (type IV) adenylyl
RT cyclase."
RL Proc. Natl. Acad. Sci. U.S.A. 88:10178-10182(1991).
CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-INSENSITIVE ADENYLYL
CC CYCLASE.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- ENZYME REGULATION: INSENSIBLE TO CA(2+)/CALMODULIN. STIMULATED BY
CC THE G PROTEIN BETA & GAMMA SUBUNIT COMPLEX.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE

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CC      FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M80633; AAA0665.1; -.
DR      PIR: A41542; A41542.
DR      HSSP: P26769; IAB8.
DR      InterPro: IPR001054; Guanylyl_cyclase.
DR      Pfam: PF00211; guanylate_cycl; 2.
DR      SMART: SM00044; CYC2; 2.
DR      PROSITE: PS00452; GUANYLATE_CYCLASES_1; 2.
DR      PROSITE: PS00125; GUANYLATE_CYCLASES_2; 2.
KW      Lyase; CAMP synthetis; Transmembrane; Glycoprotein; Duplication.
FT      DOMAIN 1 28
FT      TRANSMEM 29 50 POTENTIAL.
FT      TRANSMEM 61 80 POTENTIAL.
FT      TRANSMEM 94 117 POTENTIAL.
FT      TRANSMEM 120 138 POTENTIAL.
FT      TRANSMEM 141 162 POTENTIAL.
FT      TRANSMEM 170 190 POTENTIAL.
FT      DOMAIN 191 582 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 583 604 POTENTIAL.
FT      TRANSMEM 608 630 POTENTIAL.
FT      TRANSMEM 661 684 POTENTIAL.
FT      DOMAIN 685 707 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 708 733 POTENTIAL.
FT      TRANSMEM 741 761 POTENTIAL.
FT      TRANSMEM 788 804 POTENTIAL.
FT      DOMAIN 805 1064 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 694 694 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 1064 AA; 118798 MW; 5A2A0B895B5A0DA8 CRC64;

Query Match 10.1%; Score 72.5; DB 1; Length 1064;
Best Local Similarity 25.6%; Pred. No. 9.4;
Matches 31; Conservative 19; Mismatches 40; Indels 31; Gaps 8;

QY 4 LTRRLIALALLQLAPAPVSDPD-----APGHQKRVSMIDV--YTR--ATGQPR 50
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 235 LAEMKAETMARQAGQS--SRPENTNNHSLVYKRGQSVLYADIYGTTRLASCSPK 292
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 51 EYVVPPLTVELMG--TVANQLVPSCVTVORCGGC-----CPDDGLECVPTGOHOV 97
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 293 ELVLMIN-ELFGKFDIAKE--HECMRIKILGDCYVCVSGPLPLDPHAINCVRMGLDMC 349
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 98 R 98
DB 350 R 350

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RX      MEDLINE-98256315; PubMed-9593731;
RA      Peng J.-M., Marshall N.F., Price D.H.;
RT      Identification of a cyclin subunit required for the function of
RT      Drosophila P-TEFb.
RL      J. Biol. Chem. 273:13855-13860(1998).
CC      -1- FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR
CC      (CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION
CC      ELONGATION FACTOR B (P-TEFb), WHICH IS PROPOSED TO FACILITATE THE
CC      TRANSCRIPTION FROM ABORTIVE TO PRODUCTION ELONGATION BY
CC      PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE
CC      SUBUNIT OF RNA POLYMERASE II (RNAP II).
CC      -1- SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFb.
CC      -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
CC      -----
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CC      -----
DR      EMBL: AF051933; AAC73052.1; -.
DR      FlyBase: FBgn0025455; CYCT.
DR      InterPro: IPR000553; Cyclin.
DR      Pfam: PF00134; cyclin; 1.
DR      SMART: SM00385; CYCLIN; 2.
KW      Cyclin; Transcription regulation.
FT      DOMAIN 15 21
FT      TRANSMEM 382 390 POLY-SER.
FT      DOMAIN 426 429 POLY-SER.
FT      DOMAIN 441 449 POLY-SER.
FT      DOMAIN 553 556 POLY-SER.
FT      DOMAIN 598 603 POLY-PRO.
FT      DOMAIN 872 880 POLY-LYS.
FT      DOMAIN 993 998 POLY-GLY.
SQ      SEQUENCE 1097 AA; 118401 MW; AD55F3F57BCD3D6B CRC64;

Query Match 10.1%; Score 72.5; DB 1; Length 1097;
Best Local Similarity 24.6%; Pred. No. 9.7;
Matches 32; Conservative 19; Mismatches 36; Indels 43; Gaps 6;

QY 4 LTRRLIALALLQLAPAPVSDPD-----PGHQKRVSMIDVYTRATGCPREVVVPLTVEL 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 788 LVRSLLKES---LCPNNAISLTKRDALTMGLK-----PAEELLEPR----- 825
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 MGTVANQLVPSCVTVORCGGCCPDGIECVPTGOHOVQMQLIMIRYSSQLGEMSLSEHS 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 826 -----PAPATIRKEGIGTPMTSLASGPAP-----MDLEVPTRQAGEIKESSES 868
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 QCECRPKKKD 130
DB 869 KSE-KKKKKD 877

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RESULT 42
CCT_DROME
ID CCT_DROME STANDARD: PRT; 1097 AA.
AC 096433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin T.
GN CYCT.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Acampora D., D'Esposito M., Falella A., Pannese M., Migliaccio E.,

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RESULT 43
HXB2_HUMAN
ID HXB2_HUMAN STANDARD: PRT; 356 AA.
AC P14652; P17485; P10913;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Homeobox protein Hox-B2 (Hox-2h) (Hox-2.8) (K8).
GN HOXB2 OR HOX2H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90098876; PubMed-2574852;
RA Acampora D., D'Esposito M., Falella A., Pannese M., Migliaccio E.,

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RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
 RT "The human HOX gene family";
 RL Nucleic Acids Res. 17:10385-10402(1989).
 RN [2]
 RP SEQUENCE OF 132-208 FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-89378558; PubMed-2570724;
 RA Giampao A., Acampora D., Zappavigna V., Pannese M.,
 RA D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
 RA Simeone A., Boncinelli E., Peschle C.;
 RT Differential expression of human HOX-2 genes along the anterior-
 RT posterior axis in embryonic central nervous system";
 RL Differentiation 40:191-197(1989).
 RN [3]
 RP SEQUENCE OF 143-208 FROM N.A.
 RX MEDLINE-90215256; PubMed-2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RT "Organization of human class I homeobox genes";
 RL Genome 31:745-756(1989).
 RN [4]
 RP SEQUENCE OF 143-202 FROM N.A.
 RX MEDLINE-88329001; PubMed-2901346;
 RA Kongswan K., Webb E., Housiaux P., Adams J.M.;
 RT "Expression of multiple homeobox genes within diverse mammalian
 RT haemopoietic lineages";
 RL EMBO J. 7:2131-2138(1988).
 RN [5]
 RP SEQUENCE OF 1-42 FROM N.A.
 RX MEDLINE-95181447; PubMed-7876223;
 RA Vialle-Grojean I., Huber P.;
 RT "Transcription factor GATA-1 regulates human HOXB2 gene expression in
 RT erythroid cells";
 RL J. Biol. Chem. 270:4544-4550(1995).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
 CC 5-9 WEEKS FROM CONCEPTION.
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
 CC PROBOSCIPEDIA SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X16665; CAA34655.1; -
 DR EMBL: X16176; CAA34298.1; -
 DR EMBL: X14571; CAA32709.1; -
 DR EMBL: X78978; CAA55581.1; -
 DR PIR: S07542; M7H02H.
 DR PIR: E37042; E37042.
 DR HSSP: P14653; 1B72.
 DR TRANSFAC: T03323; -
 DR MIM: 142967; -
 DR InterPro: IPR001827; Antennapedia.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00025; ANTENNAPEDIA.
 DR SMART: SM00024; HOMEBOX.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW transcription regulation.
 FT DOMAIN 94 99 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 143 202 HOMEBOX.

FT CONFLICT 136 138 PEA -> RRL (IN REF. 2).
 SQ SEQUENCE 356 AA; 37913 MW; D7ACA0E3D5EBFB9 CRC64;
 Query Match 10.0%; Score 72; DB 1; Length 356;
 Best Local Similarity 31.8%; Pred. No. 3.5;
 Matches 27; Conservative 7; Mismatches 33; Indels 18; Gaps 5;
 QY 18 PAQAPVSPQAPAGHQKRVVSMIDYTRATQPRVVV-----PLTELMTVAQQLV 69
 DB 224 PAERPAASPGGPSASR--AAW-----EACCHPEVVGALSDPRPLVRLEGAGASS-- 274
 QY 70 PSCVTYORCGGCCPDDEGECPTGO 94
 DB 275 PGC-ALRGAGLEPGLPEDFVFSGR 298
 RESULT 44
 ID SM3C_MOUSE STANDARD; PRT; 751 AA.
 AC 062181;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 3C precursor (Semaphorin E) (Sema E).
 GN SEMA3C OR SEMAE OR SEME.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NMRT; TISSUE-Embryo;
 RX MEDLINE-95267431; PubMed-7748561;
 RA Preschel A.W., Adams R.H., Betz H.;
 RT "Nurine semaphorin D/collapsin is a member of a diverse gene family
 RT and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
 CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. MAXIMUM
 CC EXPRESSION BETWEEN DAYS 10-12 WITH MODERATE LEVELS FROM DAY 13
 CC UNTIL BIRTH.
 CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X85994; CAA59986.1; -
 DR MGD: MGI:107557; Sema3c.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003659; PSI.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00423; PSI; 1.
 KW Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 751 SEMAPHORIN 3C.
 FT DOMAIN 237 535 SEMA.
 FT DOMAIN 636 716 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 714 717 POLY-GLN.

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FT DOMAIN 724 745 ARG/LYS-RICH (BASIC).
FT DISULFID 643 709 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 751 AA: 85259 MW: A9B5995E7DBA5D8 CRC64;

Query Match 9.9%; Score 71; DB 1; Length 751;
Best Local Similarity 23.5%; Pred. No. 9.5;
Matches 28; Conservative 16; Mismatches 37; Indels 38; Gaps 5;

QY 54 VPLTVELMKTVAKQLVPSC-----VTVORC---GGCCPD-----DGLCC---V 90
DB 484 VPTTWEISSKROQLYSSNEGVSQVSLRCHITGTACDCCLPDPCAMPDGHSCSREFY 543
QY 91 PFGOHVRMQIIMIRYPSQSGEMSLSEHSQC-----ECRPKKDSAVK 134
DB 544 PFGKRRSRQDYRHGNPLTFCRGFNKATRNAAETVQGVRRNSTFLFCAPSPQASIK 602

RESULT 45
YL00_MYCFU STANDARD: PRT: 550 AA.
AC 010709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 58.9 kDa protein RV2100 precursor.
GN RV2100 OR MT2160 OR MTCY49.40.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=968295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Ruter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Emolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV3776.
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CC -----
DR EMBL: Z73966; CA98210.1; -.
DR EMBL: AE007065; AAK46441.1; ALT_INIT.
DR TIGR: MT2160; -.
DR TubercuList: RV2100; -.
DR InterPro: IPR003870; DUF222.
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR Pfam: PF02720; DUF222; 1.
DR Pfam: PF01844; HNH; 1.
DR SMART: SM00507; HNHc; 1.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 550 HYPOTHETICAL PROTEIN RV2100.
SQ SEQUENCE 550 AA: 58934 MW: B6BF18BCA1488A7CE CRC64;

Query Match 9.8%; Score 70.5; DB 1; Length 550;
Best Local Similarity 26.2%; Pred. No. 7.8;
Matches 38; Conservative 17; Mismatches 49; Indels 41; Gaps 8;

QY 8 LLLAALLQAPAPAPSPQDADPGHOKRVYSWIDY-----TRATCOPREVVVPLTVEL 60
DB 167 LLDAALEHAGAMGPLS---APLKAIDSWIDRDPGALRRSRISARTRDICIGDPDED 223
QY 61 MGTVA---KQLVPSCVTVOR-----CGCCPDGGLCEVPTGOHVRMQIIMIRYPSQSG 112
DB 224 AGTAAIMGRLYATDAAIMDRILREMAHGVCEDD-----PRTLAQR-----ADALG 269
QY 113 EMSL-EHSSQCECRPKKDSAVKPD 136
DB 270 ALAAGADHILACGCG-----KPD 286
```

Search completed: September 10, 2002, 02:57:35
Job time: 493 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 02:50:07 ; Search time 68.73 Seconds
(without alignments)
342.315 Million cell updates/sec

Title: US-09-912-436-6
Perfect score: 719
Sequence: 1 MSPLLRLRLALLQLAPAQ.....EHSQCCECRPKKDSAVKPD 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	271.5	37.8	189 6 Q95IQ4	Q95IQ4 felis silve
2	269.5	37.5	190 11 Q91ZE1	Q91ZE1 rattus norv
3	268.5	37.3	190 11 Q9QX39	Q9QX39 spalax leuc
4	264	36.7	191 4 Q96L82	Q96L82 homo sapien
5	264	36.7	191 4 Q96KJ0	Q96KJ0 homo sapien
6	264	36.7	191 4 Q95NE5	Q95NE5 macaca fasc
7	263.5	36.6	190 6 Q77643	Q77643 ovis aries
8	258	35.9	144 13 Q73822	Q73822 brachydanio
9	257	35.7	169 4 Q96NW5	Q96NW5 homo sapien
10	255	35.5	188 13 Q73682	Q73682 brachydanio
11	253	35.2	148 13 Q42571	Q42571 xenopus lae
12	253	35.2	194 13 Q42572	Q42572 xenopus lae
13	250	34.8	126 6 Q9BPP7	Q9BPP7 macaca mula
14	246.5	34.3	118 6 Q9MZB1	Q9MZB1 ovis aries
15	243.5	33.9	124 6 Q9GK00	Q9GK00 callithrix
16	234.5	32.6	142 11 Q9ERL6	Q9ERL6 mesocricetu

17	219	30.5	146 13 Q90X23	Q90X23 bothrops ja
18	200	27.8	146 13 Q90X24	Q90X24 bothrops in
19	196.5	27.3	78 6 Q9NIS2	Q9NIS2 capreolus c
20	196.5	27.3	123 6 Q9NIS1	Q9NIS1 capreolus c
21	190.5	26.5	75 6 Q18843	Q18843 oryctolagus
22	186.5	25.9	132 12 Q9YMF3	Q9YMF3 orf virus.
23	185	25.7	141 11 Q70123	Q70123 mus musculu
24	184	25.6	110 11 Q88911	Q88911 rattus norv
25	149.5	20.8	326 11 Q91ZE4	Q91ZE4 rattus norv
26	149	20.7	68 6 Q97500	Q97500 oryctolagus
27	149	20.7	418 13 Q57352	Q57352 coturnix co
28	147	20.4	326 11 Q91ZH6	Q91ZH6 meriones un
29	147	20.4	415 11 Q91ZE3	Q91ZE3 rattus norv
30	141	19.6	420 6 Q9X50	Q9X50 bos taurus
31	138	19.2	314 5 Q9BLX1	Q9BLX1 drosophila
32	138	19.2	325 5 Q96028	Q96028 drosophila
33	134.5	18.7	301 5 Q9VWP6	Q9VWP6 drosophila
34	127	17.7	118 11 Q9CU96	Q9CU96 mus musculu
35	127	17.7	196 11 Q99L56	Q99L56 mus musculu
36	127	17.7	210 6 Q29613	Q29613 felis silve
37	125	17.4	211 13 Q90WK2	Q90WK2 gallus gall
38	125	17.4	251 13 Q90W23	Q90W23 gallus gall
39	123	17.1	185 4 Q15354	Q15354 homo sapien
40	123	17.1	226 4 Q9UR23	Q9UR23 homo sapien
41	122	17.0	194 13 Q90WK1	Q90WK1 gallus gall
42	122	17.0	198 13 Q90WK3	Q90WK3 gallus gall
43	121	16.8	149 11 Q9WV07	Q9WV07 mesocricetu
44	120	16.7	211 11 Q9PUF7	Q9PUF7 gallus gall
45	115	16.0	195 13 Q9DE50	Q9DE50 brachydanio

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	189 AA.
Q95IQ4	Q95IQ4			
AC	Q95IQ4			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Koga L., Kobayashi Y., Yazawa M., Masuda K., Ohno K., Tsujimoto H.;			
RT	"Nucleotide sequence and expression of the feline vascular endothelial			
RT	growth factor."			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB071947; BAB68520.1; -			
DR	SEQUENCE 189 AA; 22193 MW; C1E4646759AB3FD6 CRC64;			

Query Match	37.8;	Score 271.5;	DB 6;	Length 189;
Best Local Similarity	43.4;	Pred. No. 2.7e-22;		
Matches 56;	Conservative 22;	Mismatches 48;	Indels 3;	Gaps 2;
QY	10 LAALLQLAPAPVSDAPGHR--KVSMDIVYATGCPREVVPLVVELMGTVAKQ 67			
DB	12 LALLLYLHHKWSGAAPMADGEHKEHREHVEFMDVYGRSYCRPIETLVLDIQEYDELEYI 71			
QY	68 LVPSCVTVORCGCCPDGECVPTGQHOVQMOLIMR-YPSOLGEMSLSEHSQCCECRP 126			
DB	72 FKPSCVPLMRGCGCNDGECVPTGQHOVQMOLIMR-YPSOLGEMSLSEHSQCCECRP 131			
QY	127 KKQDSAVKP 135			
DB	132 KKDRAKENP 140			

RESULT 2
Q91ZE1 PRELIMINARY; PRT; 190 AA.
AC Q91ZE1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN VEGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Marlon S., Lee T.-C.;
RT "Cloning of multiple VEGF splice variants from hypoxic neonatal rat
cardiomyocytes."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033506; AAL07526.1; -
SQ SEQUENCE 190 AA; 22396 MW; 58937401041F377 CRC64;

Query Match 37.5%; Score 269.5; DB 11; Length 190;
Best Local Similarity 43.8%; Pred. No. 4.6e-22;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

OY 10 LALLQLAPAPVSPDAPGHR--KYVSWIDVYTRATCCPREVVVPLTVELMGTVAKQ 67
DB 12 LALLLYLHNAKSAAPPTTEGQKAHEVVKFMDVYQRYSCRPETLVDFQETPDEIEXI 71
OY 68 LVPSCVTVQRCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCCECRP 126
DB 72 FKPSCVPLMRGCGCCNDEALCEVPTSESNTTMOIMRIKPHQSHIGEMSLFQHNKCECRP 131
OY 127 KKKSAAVKRPD 136
DB 132 KK--DRTKPE 139
RESULT 3
Q90X39 PRELIMINARY; PRT; 190 AA.
AC Q90X39;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN VEGF.
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Spalacinae;
OC Spalax.
OX NCBI_TaxID=30637;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99313148; PubMed=10386577;
RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;
RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax
ehrenbergi: the role of vascular endothelial growth factor.";
RL FEBS Lett. 452:133-140(1999).
DR EMBL; AF186236; AAD56245.1; -
DR HSSP; P15692; 2VPE.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR PRODOM; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22488 MW; 2228383BC65F0BFE CRC64;

Query Match 37.3%; Score 268.5; DB 11; Length 190;
Best Local Similarity 44.3%; Pred. No. 5.9e-22;
Matches 54; Conservative 22; Mismatches 43; Indels 3; Gaps 2;

OY 10 LALLQLAPAPVSPDAPGHR--KYVSWIDVYTRATCCPREVVVPLTVELMGTVAKQ 67
DB 12 LALLLYLHNAKSAAPPTTEGQKAHEVVKFMDVYQRYSCRPETLVDFQETPDEIEXI 71
OY 68 LVPSCVTVQRCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCCECRP 126
DB 72 FKPSCVPLMRGCGCCNDEALCEVPTSESNTTMOIMRIKPHQSHIGEMSLFQHNKCECRP 131
OY 127 KK 128
DB 132 KK 133

RESULT 4
Q96L82 PRELIMINARY; PRT; 191 AA.
AC Q96L82;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.

RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of vascular endothelial growth factor (VEGF) cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY047581; AAK95847.1; -
SQ SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;

Query Match 36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.9e-21;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

OY 10 LALLQLAPAPVSPDAPG---HQRVSWIDVYTRATCCPREVVVPLTVELMGTVAK 66
DB 12 LALLLYLHNAKSAAPPAEAGGQNHHEVVKFMDVYQRYSCRPETLVDFQETPDEIEXI 71
OY 67 QLVPSVTVQRCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCCECR 125
DB 72 IFKPSCVPLMRGCGCCNDEALCEVPTSESNTTMOIMRIKPHQSHIGEMSLFQHNKCECR 131
OY 126 PKK 128
DB 132 PKK 134

RESULT 5
Q96KJ0 PRELIMINARY; PRT; 191 AA.
AC Q96KJ0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 165B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;
RA Sugiono M., Winkler M., Gyllatt D., Harper S.J., Bates D.O.;
RT "A new isoform of vascular endothelial growth factor mRNA is down-

Query Match	Similarity	35.9%	Score 238	DB 13	Length 144
Best Local	Similarity 38.0%	Pred No. 6,4e-21			
Matches 52	Conservative 27	Mismatches 52	Indels 6	Gaps 2	
OY	5	LRRLLAALLQALAPACAPVSDPAPGHQKRVSMIDVYTRATCQPREVVPLVTLGTMGV	64		
DB	7	LTLFLTAALLHTLSAVKAAHLPKGGSKNDVIFPMVDVYKKSACKTRELIVDIQVEPDEI	66		
OY	65	ANQVPLSCVTVQRCGCCCPDDGLECVPTTQOHQVRAQIMIRIPSSQLG-EMSLIEHSGCE	123		
DB	67	EHTYTPSPCVLLKRCACCCNDEALCEVPTETRYNTEVLEVRKQVRSQHNQFSTETHTKCE	126		
OY	124	CRPK-----KDSAVKP	135		
DB	127	CRPKAEVKKAKKERCERKP	143		
RESULT	9				
O96NM5	PRELIMINARY	PRT	169 AA		
AC	O96NM5				
AD	O96NM5				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).				
GN	VEGF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
NCBI_Taxid	9606				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RP	Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,				
RL	Poel C.L., Toth E.J., Yi O., Nickerson D.A.				
DR	Submitted (OCF-2001) to the EMBL/GenBank/DBJ databases.				
FT	EMBL: AF437895; AAL27630.1; ..				
FT	NON_TER				
SO	SEQUENCE				
SO	169 AA; 19638 MW; 62832BE6EC0D6A9 CRC64;				
Query Match	35.7%	Score 257	DB 4	Length 169	
Best Local	Similarity 44.0%	Pred No. 9.8e-21			
Matches 48	Conservative 21	Mismatches 38	Indels 2	Gaps 2	
OY	21	APVSDPAPGHQKRVSMIDVYTRATCQPREVVPLVTLGTMGVAKQLVPSCVTVQRCGG	80		
DB	5	APMAEGSGGQH-HEVYKFMVDYQRSYCHPIETLDFIQEYTRDEIYFSPSCVPLMRGG	63		
OY	81	CCPDGGLCEVPTPGOHQVRAQIMIR-YPSSQLGEMSLIEHSGCECRPK	128		
DB	64	CCNDEGLECVPTESNITQIMIRKPHQGGHIGEMSFLOHNKCECRPK	112		
RESULT	10				
O73682	PRELIMINARY	PRT	188 AA		
AC	O73682				
AD	O73682				
DT	01-AUG-1998 (TREMBLrel. 07, Created)				
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR ISOFORM 165.				
GN	VEGF.				
OS	Brachydanio rerio (zebrafish) (Zebra danio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;				
OC	Cypriniformes; Cyprinidae; Danio.				
NCBI_Taxid	7955				
NCBI_Taxid	7955				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RP	MEDLINE-98222600; PubMed-9545518;				
RL	Liang D., Xu X., Chin A.J., Balasubramanian N.V., Teo M.A., Lam T.J.,				

Query	Match	Best Local Similarity	Matches	Conservative	Indels	Gaps
DB	127	CRPKAEVAKKENHCEP	143			
QY	124	CRPK-----KDSAVK	135			
DB	67	EHTYIPSCVILKRCAGCCNDEALCEVPETRYTVMEVLKRVKORVSONHNPOLSFTEHTKE	126			
QY	65	AKQIVPSCVTVYVGRGCGCCPDGLIECVPTGQOHVQMQLIMRYPSSQLG-EMSLKEHSQCE	123			
DB	7	LQQLPLAALLHLSAYKAAHIIIPKEGKSKNDVIRPNDYVKKSKARELLVDIIQEPDPI	66			
QY	5	ERRLLAALLOLAPRQAPRVSQDPARQORXKVVSMWIDVYTRATCOREVVVPLTELMTGV	64			
DB	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No. 1.8e-20;				
QY	51	Conservative	29	Mismatches	51	
QY	35.5%	Score 255;	DB 13;	Length 188;		
DB	37.2%	Pred. No				

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
35.2%, Score 253; DB 13; Length 148;	43.2%, Pred. No. 2.4e-20;	54;	21;	44;	6;	3;
10	10	10	10	10	10	10
11	11	11	11	11	11	11
12	12	12	12	12	12	12
13	13	13	13	13	13	13
14	14	14	14	14	14	14
15	15	15	15	15	15	15
16	16	16	16	16	16	16
17	17	17	17	17	17	17
18	18	18	18	18	18	18
19	19	19	19	19	19	19
20	20	20	20	20	20	20
21	21	21	21	21	21	21
22	22	22	22	22	22	22
23	23	23	23	23	23	23
24	24	24	24	24	24	24
25	25	25	25	25	25	25
26	26	26	26	26	26	26
27	27	27	27	27	27	27
28	28	28	28	28	28	28
29	29	29	29	29	29	29
30	30	30	30	30	30	30
31	31	31	31	31	31	31
32	32	32	32	32	32	32
33	33	33	33	33	33	33
34	34	34	34	34	34	34
35	35	35	35	35	35	35
36	36	36	36	36	36	36
37	37	37	37	37	37	37
38	38	38	38	38	38	38
39	39	39	39	39	39	39
40	40	40	40	40	40	40
41	41	41	41	41	41	41
42	42	42	42	42	42	42
43	43	43	43	43	43	43
44	44	44	44	44	44	44
45	45	45	45	45	45	45
46	46	46	46	46	46	46
47	47	47	47	47	47	47
48	48	48	48	48	48	48
49	49	49	49	49	49	49
50	50	50	50	50	50	50
51	51	51	51	51	51	51
52	52	52	52	52	52	52
53	53	53	53	53	53	53
54	54	54	54	54	54	54
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56	56	56	56	56	56	56
57	57	57	57	57	57	57
58	58	58	58	58	58	58
59	59	59	59	59	59	59
60	60	60	60	60	60	60
61	61	61	61	61	61	61
62	62	62	62	62	62	62
63	63	63	63	63	63	63
64	64	64	64	64	64	64
65	65	65	65	65	65	65
66	66	66	66	66	66	66
67	67	67	67	67	67	67
68	68	68	68	68	68	68
69	69	69	69	69	69	69
70	70	70	70	70	70	70
71	71	71	71	71	71	71
72	72</					

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Db 71 YIFKPSCVPLMRGAGCCNDESLCEVPTECYNTWQIMKIKPHISQHIMDSFQOHSQCEC 130
QY 125 RPKKK 129
Db 131 RPKKE 135

RESULT 12
042572 PRELIMINARY; PRT; 194 AA.
AC 042572;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 196.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBL_TaxID=8355.
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT "Neovascularization of the Xenopus embryo.";
RL Dev. Dyn. 0:0-0(1997).
DR EMBL; AF008594; AAB63680.1; -.
DR HSSP; P15692; IYGH.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR ProDom; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 194 AA; 22672 MW; 85D7BEC7CEFE17E CRC64;

Query Match 35.28; Score 253; DB 13; Length 194;
Best Local Similarity 43.28; Pred. No. 3.2e-20;
Matches 54; Conservative 21; Mismatches 44; Indels 6; Gaps 3;

QY 10 LAALLQLAPAAQAPVSPDAPG---ORKVSMIDVYTRATCOPREVVPLTVELMGTV 65
Db 12 LAVLLYLPNQLSGAP-MRGEQDHKPLEVYKFLKVIERSQVREILVDIFQEPDEVE 70
QY 66 KQLVSCVTVORCGCGCPDDGLECVPTGQHOVNRQIIMIR-YPSQLGEMSLSEHSQCEC 124
Db 71 YIFKPSCVPLMRGAGCCNDESLCEVPTECYNTWQIMKIKPHISQHIMDSFQOHSQCEC 130
QY 125 RPKKK 129
Db 131 RPKKE 135

RESULT 13
09BDP7 PRELIMINARY; PRT; 126 AA.
AC 09BDP7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBL_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hazard T.M., Nayak N.R., Jia Y., Stouffer R.L.;
RT "Rhesus macaque VEGF mRNA sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF339737; AAK26379.1; -.

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DR HSSP; P15692; ZVPF.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR ProDom; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 14599 MW; 1175F2386A83BCF CRC64;

Query Match 34.88; Score 250; DB 6; Length 126;
Best Local Similarity 42.68; Pred. No. 4.3e-20;
Matches 52; Conservative 21; Mismatches 45; Indels 4; Gaps 2;

QY 10 LAALLQLAPAAQAPVSPDAPG---ORKVSMIDVYTRATCOPREVVPLTVELMGTV 66
Db 5 LALLLYLHNAKWSQAANHAEGGQNNHNEVYKFMVYQSYCHPIETLVDFQEPDEIEY 64
QY 67 QLVPSCTVORCGCGCPDDGLECVPTGQHOVNRQIIMIR-YPSQLGEMSLSEHSQCEC 125
Db 65 IFKPSCVPLMRGCGCCNDESLCEVPTEESNTWQIMRIKPHQGHIGEMSLQHNKCECR 124
QY 126 PK 127
Db 125 PK 126

RESULT 14
09MZB1 PRELIMINARY; PRT; 118 AA.
AC 09MZB1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBL_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=PLACENTAL ARTERY ENDOTHELIUM;
RC Zhang J., Tsol S.C., Magnus R.R.;
RT "Growth factor expression in ovine fetal placental artery endothelial
cells.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250375; AAF75258.1; -.
DR HSSP; P15692; IYVP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR ProDom; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 1
SQ SEQUENCE 118 AA; 13931 MW; 757DC53AA56378A6 CRC64;

Query Match 34.38; Score 246.5; DB 6; Length 118;
Best Local Similarity 45.28; Pred. No. 9.7e-20;
Matches 47; Conservative 21; Mismatches 33; Indels 3; Gaps 2;

QY 28 APGHQR--KVVSMIDVYTRATCOPREVVPLTVELMGTVAAQVLVPSCTVORCGCGCPDD 85
Db 2 AEGGQKPREVYKFMVYQSYCHPIETLVDFQEPDEIEYIFKPSCVPLMRGCGCCNDE 61
QY 86 GLECVPTGQHOVNRQIIMIR-YPSQLGEMSLSEHSQCECRPK 128
Db 62 SLECVPTGQHOVNRQIIMIR-YPSQLGEMSLSEHSQCECRPK 105

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DR PROSITE; PSS0278; PDGF_2; 1.
 FT NON_TER 1
 RP NON_TER 75
 SQ SEQUENCE 75 AA; 8720 MW; DDC2C5B29E69359 CRC64;

Query Match 26.5%; Score 190.5; DB 6; Length 75;
 Best Local Similarity 55.9%; Pred. No. 9.6e-14;
 Matches 33; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 7C PSCVTQVRCGCGCCPDGECVPTGQHVYRMOILMIR-YPS5QIGEMSLSEHSQCECRP 127
 DB 17 PSCVPLVRGCGCCNDSELCVPTEEFVNTQIMRIKPHQGHIGEMSEIQHNKCECRP 75

RESULT 22
 Q9YMF3 PRELIMINARY; PRT; 132 AA.

AC Q9YMF3; 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG VEGF-E.
 OS orf virus
 OC viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Parapoxvirus.
 OX NCBI_Taxid=10258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D1701;
 RX MEDLINE=99107753; PubMed=9889193;
 RA Meyer M., Claus M., Lepple-Wienhues A., Waltenberger J.,
 RA Augustin H.G., Ziche M., Ianz C., Buettner M., Rziha H.J., Dehio C.;
 RT "A novel vascular endothelial growth factor encoded by orf virus.
 RT VEGF-E, mediates angiogenesis via signalling through VEGFR-2 (KDR) but
 RT not VEGFR-1 (Flt-1) receptor tyrosine kinases."
 RL EMBO J. 18:363-374(1999).
 DR EMBL; AF106020; AAD03735.1; -.
 DR HSSP; P15692; 1VPP.
 DR InterPro; IPR000072; PDGF.
 DR Pfam; PF00341; PDGF; 1.
 DR ProDom; PD001629; PDGF; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS0278; PDGF_2; 1.
 SQ SEQUENCE 132 AA; 14763 MW; 15F403A06B872926 CRC64;

Query Match 25.9%; Score 186.5; DB 12; Length 132;
 Best Local Similarity 36.3%; Pred. No. 4.9e-13;
 Matches 33; Conservative 20; Mismatches 37; Indels 1; Gaps 1;

QY 37 SMIDVYTRATCCPREVYVFLVLMGTAKQLVPSCVTVQRCGCGCCPDGECVPTGQHV 96
 DB 25 TISEVFENSGCKRPVYVHDEHPRLTSQRFPPCVTLIRGCGCCNDSELCVPTGEAN 84

QY 97 VEMOILMIRYPS5Q-IGEMSLSEHSQCECRP 126
 DB 85 VTMQLMGASVSGNGMQLHSLFVEHKKCDCKP 115

RESULT 23
 ID 070123 PRELIMINARY; PRT; 141 AA.

AC 070123; 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE VEGF115.
 GN VEGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR.

RX MEDLINE=95101726; PubMed=7803491;
 RA Sugihara T., Kaul S.C., Mitsui Y., Wadhwa R.;
 RT "Enhanced expression of multiple forms of VEGF is associated with
 RT spontaneous immortalization of murine fibroblasts."
 RL Biochim. Biophys. Acta 1224:365-370(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ICR;
 RX MEDLINE=98112857; PubMed=9446618;
 RA Sugihara T., Wadhwa R., Kaul S.C., Mitsui Y.;
 RT "A novel alternatively spliced form of murine vascular endothelial
 RT growth factor, VEGF 115."
 RL J. Biol. Chem. 273:3033-3038(1998).

DR EMBL; U50279; AAC05442.1; -.

DR HSSP; P15692; 1VPP.

DR MGD; MGI:103178; Vegf.

DR InterPro; IPR000072; PDGF.

DR Pfam; PF00341; PDGF; 1.

DR ProDom; PD001629; PDGF; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.

SQ SEQUENCE 141 AA; 15550 MW; A27C4EF5A7071338 CRC64;

Query Match 25.7%; Score 185; DB 11; Length 141;
 Best Local Similarity 39.4%; Pred. No. 7.7e-13;
 Matches 37; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

QY 10 LAILDLAPAAQAVSOPDAPGHR--KYVSMIDVYTRATCCPREVYVFLVLMGTAVAK 67
 DB 12 LAILTLHRAKSSQAAPTEBGEQKSHVTKEMVYORSYCRPLETVDTIIOETPEIEYI 71

QY 68 LVPSCVTVQRCGCGCCPDGECVPTGQHVYRMOI 101
 DB 72 FRPSCVPLMRGCGCCNDSELCVPTSESNTMVO 105

RESULT 24
 ID 088911 PRELIMINARY; PRT; 110 AA.

AC 088911; 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR A 110 (FRAGMENT).

GN VEGF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=PENIS;

RX MEDLINE=99115228; PubMed=9916007;

RA Burchard M., Burchard T., Chen M.W., Shabsigh A., de la Taille A.,

RA Butyran R., Shabsigh R.;

RT "Expression of messenger ribonucleic acid splice variants for vascular

RT endothelial growth factor in the penis of adult rats and humans."

RL Biol. Reptod. 60:398-404(1999).

DR EMBL; AF080594; AAC36708.1; -.

DR HSSP; P15692; 1VPP.

DR InterPro; IPR000072; PDGF.

DR Pfam; PF00341; PDGF; 1.

DR ProDom; PD001629; PDGF; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.

FT NON_TER 1

SQ SEQUENCE 110 AA; 12713 MW; B81B79AC08D89F06 CRC64;

Query Match 25.6%; Score 184; DB 11; Length 110;
Best Local Similarity 34.2%; Pred. No. 7.6e-13;
Matches 39; Conservative 15; Mismatches 38; Indels 22; Gaps 2;

OY 21 APVSOPDAGHOKKRVSMIDYTRATCOPREVVPPLTVELMGVAQOLVPSCTVQRCGG 80
DB 1 APTTEGQRAHE--VVKEMDVQRSYCRPETLVDFIQEPDEIEYIFKPSCVPLMRACAG 58

OY 81 CSDPDDLECVPTGQHOVRMQLMIRYPSOLGEMSLSEHSQCECRPKKSAVK 134
DB 59 CCNDELCEVPISSENVTMQ-----TCCKSCKNDSRCK 92

RESULT 25
OY1ZE4 PRELIMINARY; PRT: 326 AA.

AC OY1ZE4

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE VEGF-D.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OK NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY;

RA Kiriln V., Maritschek R., Krishnan J., Steffen A., Waltenberger J.,

Pepper M.S., Giansis A., Sleeman J.P.;

RT "Characterization of indolinones which specifically inhibit VEGF-C and

VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";

RL Eur. J. Biochem. 0:0-0(2001).

DR EMBL; AY032728; AAK96008.1;

SQ SEQUENCE 326 AA; 37106 MW; D7CAEBA6C9FAB7D CRC64;

Query Match 20.8%; Score 149.5; DB 11; Length 326;

Best Local Similarity 32.3%; Pred. No. 1.6e-08;

Matches 31; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

OY 34 KYVSMIDYTRATCOPREVVPPLTVELMGVAQOLVPSCTVQRCGGCCPDGCEVPTG 93

DB 105 KYID--EEMQRTQCSPRECEVASELGTNTTFKPPCVNPRCGGCCNEESVMCMNTS 162

OY 94 OHQVRMQLMIRYPSOLGEM--SLSEHSQCECRP 126

DB 163 TSYISKQLEISVPLTSVELVAVKIANHTGCKLP 198

RESULT 26
OY7500 PRELIMINARY; PRT: 68 AA.

AC OY7500

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
FT NON_TER 1 68
SQ SEQUENCE 68 AA; 7819 MW; 687638661E98DE0 CRC64;

Query Match 20.7%; Score 149; DB 6; Length 68;
Best Local Similarity 47.5%; Pred. No. 3.4e-09;
Matches 28; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

OY 47 COPREVVPPLTVELMGVAQOLVPSCTVQRCGGCCPDGCEVPTGQHOVRMQLMIR 105
DB 6 COPLETLVDIFQEPDEIEYIFKPSCVPLVRGCGCCNDELCEVPTEEFVMTQIMRIK 64

RESULT 27

OY7352 PRELIMINARY; PRT: 418 AA.

AC OY7352

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.

GN VEGF-C.

OS Columba coturnix (common quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Columba.

OK NCBI_TaxID=9091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98167900; PubMed=9435294;

RA Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,

Altalo K., Le Douarin N.M.;

RT "Avian VEGF-C: cloning, embryonic expression pattern and stimulation

of the differentiation of VEGFR2 expressing endothelial cell

precursors.";

RL Development 125:743-752(1998).

DR EMBL; Y15837; CA75799.1;

DR HSSP; P15692; IVP.

DR InterPro: IPR004153; CXXC.

DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR000072; PDGF.

DR Pfam: PF003128; CXXC; 6.

DR Pfam: PF00341; PDGF; 1.

DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00067; GHA; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
KW signal.
FT CHAIN 1 31
SQ SEQUENCE 418 AA; 46839 MW; 099BFC79151BF2B CRC64;

Query Match 20.7%; Score 149; DB 13; Length 418;

Best Local Similarity 31.7%; Pred. No. 2.4e-08;

Matches 33; Conservative 16; Mismatches 51; Indels 4; Gaps 2;

OY 28 APGHOKRVSMIDYTRAT--COPREVVPPLTVELMGVAQOLVPSCTVQRCGGCCPDG 86

DB 110 AAHYNELIKSLDTEWKKTCMPRECVDGKEGATTTTFKPPCVSITRCGCSSEG 169

OY 87 LECVPTGQHOVRMQLMIRYPSOLGEM--MSLEHSQCECRPK 127

DB 111 418 VASCULAR ENDOTHELIAL GROWTH FACTOR C.

FT CHAIN 1 31

SQ SEQUENCE 418 AA; 46839 MW; 099BFC79151BF2B CRC64;

Db 170 LQCMNTSTGYLSKTLFEITVPLSGPKPVTYSFANHNSCRMSK 213

RESULT 28

0912H6 PRELIMINARY; PRT: 326 AA.

AC 0912H6: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C (FRAGMENT).

GN VEGFC.

OS Meriones unguiculatus (Mongolian jird).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

OX NCBI_TaxID=10047;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RA Panlailais B.J., Fuhrman J.A.;

RT "Brugia malayi stimulates VEGF-C, a growth factor specific for lymphatic endothelium, by an indirect mechanism."

RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF432867; AAL28127.1; -.

FT NON_TER 1

SQ SEQUENCE 326 AA; 36826 MW; DOB2772C77836914 CRC64;

Query Match 20.4%; Score 147; DB 11; Length 326;

Best Local Similarity 32.7%; Pred. No. 3,1e-08;

Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

Db 18 AAHYNTETLKSIDNEMWRTQCMPEVCIIDVGKEFGAATNTEFFKPCVSVYRCGCCNSEG 77

QY 87 LECVPTGQHVQMOLIMIRPSSQGE--MSLEHSCCECRPK 127

Db 78 LQCMNTSTGYLSKTLFEITVPLSGPKPVTYSFANHNSCRMSK 121

RESULT 29

0912E3 PRELIMINARY; PRT: 415 AA.

AC 0912E3: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

OS VEGF-C.

DE Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY;

RA Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

RA Pepper M.S., Giannis A., Sleeman J.P.;

RT "Characterization of indolinones which specifically inhibit VEGF-C and VEGF-D-induced activation of VEGFR-3 but not VEGFR-2."

RT EMBL; AY032729; AAK96009.1; -.

DR EMBL; AY032729; AAK96009.1; -.

SQ SEQUENCE 415 AA; 46397 MW; 1EB677F5B260A525 CRC64;

Query Match 20.4%; Score 147; DB 11; Length 415;

Best Local Similarity 32.7%; Pred. No. 4e-08;

Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

Db 28 APGHQRKVVSMIDVYTRAT-CQPREVVVPLTVELMGTVAKQLVPSCVTVORCGCCPDG 86

QY 107 AAHYNTETLKSIDNEMWRTQCMPEVCIIDVGKEFGAATNTEFFKPCVSVYRCGCCNSEG 166

QY 87 LECVPTGQHVQMOLIMIRPSSQGE--MSLEHSCCECRPK 127

Db 167 LQCMNTSTGYLSKTLFEITVPLSGPKPVTISFANHNSCRMSK 210

RESULT 30

09XS50 PRELIMINARY; PRT: 420 AA.

AC 09XS50: 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

CC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART;

RA MEDLINE=20044783; PubMed=10575000;

RA Yonekura H., Sakurai S., Liu X., Migita H., Wang H., Yamagishi S.,

RA Nomura M., Abedin M.J., Uno K. H., Yamamoto Y., Yamamoto H.;

RT "Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes."

RT Implication in autocrine and paracrine regulation of angiogenesis.";

RT J. Biol. Chem. 274:35172-35178(1999).

DR EMBL; AB004275; BAA77687.1; -.

DR HSSP; P15692; IVP.

DR InterPro; IPR004153; CXXC.

DR InterPro; IPR000072; PDGF.

DR Pfam; PF00341; PDGF_1.

DR Pfam; PD001629; PDGF_1.

DR SMART; SM00141; PDGF_1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS50278; PDGF_2; 1.

KW SIGNAL.

FT SIGNAL 1 20 POTENTIAL.

FT CHARIN 21 420 VASCULAR ENDOTHELIAL GROWTH FACTOR C.

SQ SEQUENCE 420 AA; 46681 MW; 58BA84317A3C8E2D CRC64;

Query Match 19.6%; Score 141; DB 6; Length 420;

Best Local Similarity 31.7%; Pred. No. 1,9e-07;

Matches 33; Conservative 15; Mismatches 52; Indels 4; Gaps 2;

QY 28 APGHQRKVVSMIDVYTRAT-CQPREVVVPLTVELMGTVAKQLVPSCVTVORCGCCPDG 86

Db 112 AAHYNTETLKSIDNEMWRTQCMPEVCIIDVGKEFGAATNTEFFKPCVSVYRCGCCNSEG 171

QY 87 LECVPTGQHVQMOLIMIRPSSQGE--MSLEHSCCECRPK 127

Db 172 QQCMNTSTGYLSKTLFEITVPLSGPKPVTISFANHNSCRMSK 215

RESULT 31

09BLX1 PRELIMINARY; PRT: 314 AA.

AC 09BLX1: 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PDGF/VEGF FACTOR-1 PRECURSOR.

GN PVF1.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

CC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

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RP SEQUENCE FROM N.A.
RA Heino T.I., Wahlstroem G., Kaerpenen T., Pulkkinen M., Allitalo K.,
RT Roos C.;
RA "Drosophila PDGF/VEGF receptor homolog is specifically expressed in
RT hemocytes.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ401391; CAC24699.1; -
DR InterPro: IPR004153; CXKCX.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF03128; CXKC; 3.
DR Pfam: PF00341; PDGF; 1.
DR PRODOM: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KM Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SQ SEQUENCE 314 AA; 34482 MW; DE7771E7B2BD5EDD CRC64;

Query Match 19.2%; Score 138; DB 5; Length 314;
Best Local Similarity 26.9%; Pred. No. 2.9e-07;
Matches 39; Conservative 29; Mismatches 61; Indels 16; Gaps 5;

QY 2 SPLRLRLALLQLAPQAQAPVS--QPDAPGHORQVY--SWIDVYTRATCOPREVVVPLT 57
DB 82 TPLRLPLSVSELTNTVADYVSGEMPSSEKFNKSIYRNATPASCSPQPIVEIK 141
QY 58 VELMGTVAKOLVPSCVTYVQRCGGCCPDGELCEVPTGQHOVRMQLMI-----RYPSSQ 110
DB 142 PPAEDENAYYYMPACTRISRCNGCCGSLISQCPTEVQVQVRKVKVRAATSGRRPPTI 201
QY 111 LGEMSLERHSQ--CECRPKKDSAY 133
DB 202 I---TVEQHTQCRDCRTRKAEKCNV 223

RESULT 32
QY 096028 PRELIMINARY; PRT; 325 AA.
AC 096028;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LD28763P.
GN CG7103.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Abbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacl J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY051751; AAK93175.1; -
DR SEQUENCE 325 AA; 35779 MW; D215BC47DCAAFDPD CRC64;

Query Match 19.2%; Score 138; DB 5; Length 325;
Best Local Similarity 26.9%; Pred. No. 3e-07;
Matches 39; Conservative 29; Mismatches 61; Indels 16; Gaps 5;

QY 2 SPLRLRLALLQLAPQAQAPVS--QPDAPGHORQVY--SWIDVYTRATCOPREVVVPLT 57
DB 93 TPLRLPLSVSELTNTVADYVSGEMPSSEKFNKSIYRNATPASCSPQPIVEIK 152
QY 58 VELMGTVAKOLVPSCVTYVQRCGGCCPDGELCEVPTGQHOVRMQLMI-----RYPSSQ 110

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DB 153 PPAEDENAYYYMPACTRISRCNGCCGSLISQCPTEVQVQVRKVKVRAATSGRRPPTI 212
QY 111 LGEMSLERHSQ--CECRPKKDSAY 133
DB 213 I---TVEQHTQCRDCRTRKAEKCNV 234

RESULT 33
QY 09VWP6 PRELIMINARY; PRT; 301 AA.
AC 09VWP6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG7103.
DE CG7103 PROTEIN.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BERKELEY;
RC MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazel R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abtil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalaali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekriov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacl J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
DR EMBL: AE003510; AAF4892.2; -
DR FLYBase: FBgn0030964; Pvfl.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR PRODOM: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR SEQUENCE 301 AA; 33013 MW; 4C45D988AAC9A5A9 CRC64;

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RA MEDLINE=86120370; PubMed=3003695;
RA van den Ouweland A.M.W., Roebroek A.J.M., Schalken J.A.,
RA Claassen C.A.A., Bloemers H.P.J., Van de Ven W.J.M.,
RT "Structure and nucleotide sequence of the 5' region of the human and
RT feline c-sis proto-oncogenes."
RL Nucleic Acids Res. 14:765-778(1986).
DR EMBL; X06297; CAA29623.1; -
DR EMBL; X06298; CAA29623.1; JOINED.
DR EMBL; X06299; CAA29623.1; JOINED.
DR EMBL; X06300; CAA29623.1; JOINED.
DR EMBL; X06301; CAA29623.1; JOINED.
DR EMBL; X06302; CAA29623.1; JOINED.
DR EMBL; X03494; CAA27210.1; -
DR EMBL; M25358; AAA30817.1; JOINED.
DR EMBL; M25357; AAA30817.1; JOINED.
DR EMBL; M25353; AAA30817.1; JOINED.
DR EMBL; M25354; AAA30817.1; JOINED.
DR EMBL; M25355; AAA30817.1; JOINED.
DR HSSP; P01127; 1PDG.
DR InterPro: IPR002400; GE_CysKnot.
DR InterPro: IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GE_CYSKNOT.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 210 AA; 23649 MW; CDD19FBA1A04C1E6 CRC64;

Query Match 17.7%; Score 127; DB 6; Length 210;
Best Local Similarity 34.8%; Pred. No. 3.2e-06;

Matches 31; Conservative 18; Mismatches 28; Indels 12; Gaps 4;

QY 45 ATCOPREVYVPLVELMG-TVAKOLV-PSCVTYORCGCCCPDDGLECVPTGQHOVMQIL 102
DB 99 AECKTRTEVEVSRILDRNANFLVWPCEVYORCGCCNNRNVCQRP---QVQLRLV 155
QY 103 MIR-----YPSQUGEMSLFHSQCEC 124
DB 156 QVRKIEIVRRKRPVKATVLEDLHACK 184

RESULT 37
Q90WK2 PRELIMINARY; PRT; 211 AA.
AC Q90WK2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR A CHAIN LONG FORM PRECURSOR.
GN PDGF-A (L).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363439; PubMed=11470524;
RA Horuchi H., Inoue T., Furusawa S., Matsuda H.,
RT "Characterization and expression of three forms of cDNA encoding
RT chicken platelet-derived growth factor-A chain."
RL Gene 272:181-190(2001).
DR EMBL; AB031022; BAB62541.1; -
KM Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 87 211 PDGF-A LONG FORM.
SQ SEQUENCE 211 AA; 24380 MW; D3DDE8E32BE43B08 CRC64;

Query Match 17.4%; Score 125; DB 13; Length 211;

Best Local Similarity 28.8%; Pred. No. 5.3e-06;
Matches 34; Conservative 20; Mismatches 36; Indels 28; Gaps 6;

QY 45 ATCOPREVYVPLVELMGTVAKOLV-PSCVTYORCGCCCPDDGLECVPTGQHOVMQIL 101
DB 94 AECKTRTEVEVSRILDRNANFLVWPCEVYORCGCCNNRNVCQRP---QVQLRLV 152
QY 102 LMIRY-----PSSQUGEMSLFHSQCEC-----RP-----KKKDSAVKP 135
DB 153 AKVEIVRRKPKLKEVLVLEHMECTCTSTNTSDYREETGRPRESGKKRKKRKLKP 210

RESULT 38
Q90WK2 PRELIMINARY; PRT; 251 AA.
AC Q90WK2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR B CHAIN PRECURSOR.
GN PDGF-B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHRON;
RA Horuchi H., Inoue T., Furusawa S., Matsuda H.,
RT "Cloning and characterization of a chicken platelet-derived growth
RT factor-B chain cDNA."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB031025; BAB64507.1; -
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 88 196 PDGF-B.
SQ SEQUENCE 251 AA; 28515 MW; 52B096C938C4298A CRC64;

Query Match 17.4%; Score 125; DB 13; Length 251;
Best Local Similarity 30.0%; Pred. No. 6.4e-06;
Matches 30; Conservative 20; Mismatches 34; Indels 16; Gaps 4;

QY 45 ATCOPREVYVPLVELMGTVAKOLV-PSCVTYORCGCCCPDDGLECVPTGQHOVMQIL 102
DB 102 AECKTRTEVEVSRILDRNANFLVWPCEVYORCGCCNNRNVCQRP---QVQLRLV 158
QY 103 MIR-----YPSQUGEMSLFHSQCEC---RPPKKDS 131
DB 159 QVNRTEFFQRPFKKYVPLEDHVQRCCEVSRPPRSN 198

RESULT 39
Q15354 PRELIMINARY; PRT; 185 AA.
AC Q15354;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF 2 PROTEIN (FRAGMENT).
GN ORF 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RX MEDLINE=95388493; PubMed=7659502;
RA Dirks R.P.H., Onnekink C., Jansen H.J., de Jong A., Bloemers H.P.J.,
RT "A novel human c-sis mRNA species is transcribed from a promoter in c-
sis intron 1 and contains the code for an alternative PDGF B-like

[illegible]

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DB 94 AVCKTRVYIEIPRS-QIDPISANFLIWPCEVVKRGTGCGTSCNTSVKQCPSPRIHHSVKY 152
QY 102 LMIRY----PSSQLGEMSLSEHSQCCECRPKKDS 131
DB 153 AKVEYVRKKPKLKEVLRLEEHMECTCTSTINTNS 186

RESULT 43
Q9WV07 PRELIMINARY; PRT; 149 AA.
AC Q9WV07;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE PDGF A (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB028637; BAA78768.1; -.
DR HSSP; P01127; 1PDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 149
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16963 MW; C93814FA6D041A65 CRC64;

Query Match 16.8%; Score 121; DB 11; Length 149;
Best Local Similarity 31.3%; Pred. No. 1e-05;
Matches 31; Conservative 18; Mismatches 38; Indels 12; Gaps 5;

QY 45 ATGCPREVV--VPLTVELMGTVAKOLY-PSCVTVORCGCCPDGGLCEVPTGQHVQWMOI 101
DB 53 AVCKTRVYIEIPRS-QADPTSANFLIWPCEVVKRGTGCGTSCNTSVKQCPSPRIHHSVKY 111
QY 102 LMIRY----PSSQLGEMSLSEHSQCCECRPKKDSAVKPD 136
DB 112 AKVEYVRKKPKLKEVLRLEEHMGCTC---ATSNLNPD 146

RESULT 44
Q9PUF7 PRELIMINARY; PRT; 211 AA.
AC Q9PUF7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR A-CHAIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302546; PubMed=10842055;
RA Ataliois P.;
RT "Platelet-derived growth factor A modulates limb chondrogenesis both
in vivo and in vitro."
RL Mech. Dev. 94:13-24(2000).
DR EMBL: AF188841; AAF01459.1; -.
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DR HSSP; P01127; 1PDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 211 AA; 24349 MW; 1A6AA3A5DBD42382 CRC64;

Query Match 16.7%; Score 120; DB 13; Length 211;
Best Local Similarity 30.9%; Pred. No. 1.9e-05;
Matches 29; Conservative 18; Mismatches 39; Indels 8; Gaps 4;

QY 45 ATGCPREVV--VPLTVELMGTVAKOLY-PSCVTVORCGCCPDGGLCEVPTGQHVQWMOI 101
DB 94 AVCKTRVYIEIPRS-QIDPISANFLIWPCEVVKRGTGCGTSCNTSVKQCPSPRIHHSVKY 152
QY 102 LMIRY----PSSQLGEMSLSEHSQCCECRPKKDS 131
DB 153 AKVEYVRKKPKLKEVLRLEEHMECTCTSTINTNS 186

RESULT 45
Q9DE50 PRELIMINARY; PRT; 195 AA.
AC Q9DE50;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR A CHAIN.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu L.; Balasubramanian N.V.; Ge R.;
RT "The zebrafish PDGF-A/PDGF-R-alpha signalling system in early
embryogenesis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200950; AAG43478.1; -.
DR HSSP; P01127; 1PDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 195 AA; 22618 MW; 49B25831E1975604 CRC64;

Query Match 16.0%; Score 115; DB 13; Length 195;
Best Local Similarity 29.4%; Pred. No. 6.2e-05;
Matches 30; Conservative 22; Mismatches 40; Indels 10; Gaps 6;

QY 31 HOKRVSNIDVYIRATQCPREVV--VPLTVELMGTVAKOLY-PSC-VTVORCGCCCPDDG 86
DB 80 HSRKRS-IEAVPAVCKTRVYIEIPRS-QVDTANFLIWPCEVVKRGTGCGTSCNTSN 137
QY 87 LECVPTGQHVQWMOILMIRY----PSSQLGEMSLSEHSQCCEC 124
DB 138 MRCHPSKKHHRNVKAVKVEYVRKKPKLKEVLRLEEHMECTCTSTINTNS 179
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Job time: 539 sec

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